## Energy Research and Development Division FINAL PROJECT REPORT

# ADVANCED MODELING OF THE BIOLOGICAL EFFECTS OF CLIMATE CHANGE AND LAND USE PLANNING IN CALIFORNIA

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Advanced Modeling of the Biological Effects of Climate Change and Land Use Planning in California is the final report for the Advanced Modeling of the Biological Effects of Climate Change and Land Use Planning in California project (contract number 500-08-020) conducted by Conservation International and University of California Santa Barbara. The information from this project contributes to Energy Research and Development Energy-Related Environmental Research Program.

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#### **ABSTRACT**

Climate change is causing shifts in species' ranges and the timing of biological events worldwide. These biological events coupled with extensive physical alterations form part of the evidence base for human-induced climate change. These changes cause fundamental challenges to biological systems that affect conservation and management systems, posing threats including changes in fire regimes and extinction risk. A new generation of research tools is emerging to help improve the understanding of these threats and how to handle them. Researchers are developing tools to better understand system dynamics and the possible effects of micro-climates and fine-scale changes. These tools represent significant advances over firstgeneration climate change biology models, which were generally static and coarse scale (tens to hundreds of kilometers). This report summarized progress made in developing three new types of tools for dynamic and fine-scale biological modeling. Fine-scale models were developed on scales of tens of meters for the first time for California plant species. These models were tested against models at scales of hundreds of meters and kilometers and significant differences were detected. A conservation planning tool known as Network Flow analysis was refined to run using large numbers of species, allowing identification of important conservation areas taking into consideration more than 1,000 native California plant species. A dynamic modeling tool called BioMove was further enhanced to simulate California fire regimes. These advances helped provide tools for California's conservationists and land managers to plan for climate change. They were made publicly available on a website, allowing easy access for professionals wishing to learn how to use them or to access the thousands of plant species distribution models that were prepared for use with these tools.

**Keywords:** Climate change, fine-scale, emissions scenarios, fire, species distribution modeling, dynamic species modeling, Network Flow, BioMove, land use, conservation

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#### **EXECUTIVE SUMMARY**

#### Introduction

Climate change is modifying the geographic distributions of certain plant species within the state. General warming trends are shifting these plant species upslope and higher in elevation. Plants species are exhibiting more complex responses where precipitation change and species interactions have strong influence on their ranges. In the past, species responses to climate change have included persistence or movement that was mediated by microclimates that were quite different than normal regional climates. Species also moved over large distances in response to climate changes similar in magnitude to those expected this century. Each species' response to the effects of climate change was individualistic - different species moving at different paces - creating new plant assemblages.

Fine-scale climatic influences on plant responses to climate change were indicate by evidence that small areas of protected habitat called micro refuges allowed forest areas to exist close to the ice sheets at the last glacial maximum. These small patches of forest allowed rapid plant response to the warming temperatures as the last ice age waned. Rapid colonization by plants of recently deglaciated areas most likely came from these refuges, rather than from long-distance dispersal from warmer areas. Simulating these unusual micro-climates is important to understand future plant responses to human-induced warming. Until recently, future climate projections were only available at scales of kilometers or tens of kilometers, too coarse to capture the micro-climates and small forest patches important in the past, which existed at scales of tens or hundreds of meters.

Just as they have done in the past, plant species are expected to move long distances in response to future climate change. Past climate change has moved species' ranges over broad distances and migrations on a continental or regional scale were common. Large elevation gradients in mountains have led to large temperature gradients that compressed the migration areafor many species.. These latitudinal and elevational shifts pose a serious problem for conservation. How can species be safeguarded while migrating if protected areas are fixed in place?

#### **Project Purpose**

This project developed tools that would help conservationists and land use managers simulate climate change effects on natural vegetation and ecosystem services in California.

#### **Project Results**

To advance the dynamic and fine-scale biological modeling of species' responses to climate change, three new types of tools were developed . These models were applied to California and the results illustrate the types of applications where these tools may prove useful, and provides a starting point for more detailed studies of specific climate change issues or regions.

For the first time, high resolution models scales of tens of meters were developed to simulate the role of fine-scale climatic variations in California plant species responses to climate change.. The Species Distribution Models (SDM) were tested against models at scales of hundreds of meters and kilometers and found significant differences at multiple scales (90 meters, 270

meters, 800 meters, four kilometers and 16 kilometers). This effort required developing and accessing fine-scale climate projections and applying them in models of species'responses to climate change. A working group of biologists and climatologists developed the underlying fine-scale theory and produced the appropriate models for multiple species. This project also leveraged a major investment by the National Science Foundation in a multi-year, \$3 million effort to extend and deepen the efforts of the working group.

The previously developed Network Flow tool can help address the challenge of protecting species undergoing migration when protected areas were fixed in place, but this model had only been applied in small areas with limited numbers of species. In this research effort, Network Flow was refined and adapted for California's large land areas and unique biodiversity, taking into account more than 1,000 native California plant species to identify important conservation areas.

In this research, Network Flow is shown to be a useful tool in analyzing climate change effects for an area as large and floristically diverse as California. The use of this tool also shows that there are priority areas for conservation that can improve the protection of California's plant species as the climate changes. Refinements to Network Flow also greatly speeded up model runs for planning applications, reducing run times from days or weeks to hours. This refined tool could be applied to many other biologically significant areas, such as other global biodiversity hotspots or any large region, where climate change planning must be undertaken for numerous species.

This research study also refined BioMove, a dynamic species-based climate change modeling tool. The importance of species-based models is indicated by past evidence that individual species respond to climate change rather than plant communities. In response to climate change, each specie moves in their own unique way by tracking the climatic conditions suitable for survival and growth. This individual species response necessitates the need for models that can simulate the fate of individual species under climate change, such as BioMove. BioMove which was developed under a previous Energy Commission grant, simulates individual species movements in response to climate change in a dynamic way, incorporating competition with other species and the role of disturbances, such as fire. This project expands the library of species simulations with BioMove and improves the understanding of how to incorporate the effects of fire into simulations of plant responses to climate change.

The advances in BioMove included modeling at finer resolutions, modeling of additional species, and improved simulation of the effects of fire. The authors tested BioMove at a 270 meter grain, which is an approximately 10-fold increase in horizontal resolution. This expanded resolution allowed BioMove dynamic simulations to match the fine-scale static simulations of the species distribution models. The library of species addressed by BioMove was expanded significantly, an important advance because the data needed to parameterizean individual species is a substantial effort. Researchers worked with California fire specialists to improve simulation of fire impacts on species response to climate change in BioMove.

#### **Project Benefits**

Understanding management and conservation issues associated with climate change require research methods and tools that are able to address species dynamics and the individualistic nature of species' responses. The alterations of species' ranges due to climate change have major repercussions for conservation and land management. Attempts to protect species from extinction are complicated when species' locations are shifting. Land use management, such as tourism or fire control, may be affected by shifting species compositions, particularly those plants that provide ecosystem structure.

The modeling tools and conceptual advances developed in this project provided California land managers and conservationists with an important new set of tools to assess the dynamics of species and how they respond to climate change. These tools also benefit electricity utilities and their ratepayers with high resolution tools to identify how climate change and plant species response will affect energy infrastructure, such as transmission lines and the potential for wildfires as well as vegetation changes within watersheds and that effect on runoff and hydropower generation.

These tools were made publicly available on a website, allowing easy access for professionals to learn how to use them or to access the thousands of plant species distribution models that were prepared for use with these tools. Thousands of species models were also made available online. Further refinement and application of these tools to address real-world problems could make California a leader in dynamic, spatially-explicit planning of conservation and land use to adapt to climate change.

### **CHAPTER 1:** Introduction

#### 1.1 Background

Climate change is changing geography for plant species and ecosystems (Parmesan and Yohe, 2003; Root et al. 2003). Species ranges are shifting upslope and higher in elevation responding to general warming trends, and are exhibiting more complex responses where precipitation change and species interactions have strong influence. Simulations by biological models driven by global climate models (GCM), indicate that plant range changes can be expected to continue and intensify with human-induced climate change this century.

These shifts in species' ranges due to climate change have major repercussions for conservation and land management. Attempts to protect species from extinction are complicated when species' locations are changing. Land use management, such as tourism or fire control, may be affected by shifting species compositions, particularly those plants that provide ecosystem structure.

Understanding management and conservation issues associated with climate change require research methods and tools that are able to address species dynamics and the individualistic nature of species' responses. Paleoecology studies make clear that species move in response to climate change in ways that reflect unique species' climatic tolerances. This results in species moving independent from one another, or individualistically. This individualistic movement means that plant communities do not move in unison, but rather disassemble and reassemble depending on the movement of their component (plant species) parts.

Tracking species movement in response to climate change, and understanding of individualistic range shifts, is a major focus of current research in climate change biology. Species distribution modeling (SDM; also known as bioclimatic envelope modeling, or niche-based modeling) has found a central role in this effort. The primary strength of SDM is its reliance on the concept of the ecological niche (Grinnell 1917; Hutchinson 1959) and the abundance of data that can be used to derive the niche. Any observation of a species' occurrence that is associated with good locational data (georeferencing) can be used in SDM. These models then establish a statistical-(e.g., GLM, GAM) or machine learning- (e.g., MaxEnt) based association between occurrence points and current climate. That relationship can then be used to infer species distributions under future climates, using climatic conditions derived from global climate model (General Circulation Model – GCM) simulations (e.g. Heikkinen et al. 2006; Pearson and Dawson 2003; Thuiller 2003).

While SDM have been recognized as a valuable tool for understanding future biological responses to climate change, they also have a number of well-recognized limitations. Among these limitations are that SDM are typically implemented at scales that are very coarse relative to the climates experienced by individual plants, that species interactions and disturbance are ignored, and that the focus on individual species, while biologically well-justified, makes it

difficult to draw conclusions for conservation or management that encompass many dozens or hundreds of species.

Recognizing this, previous work in this lab under the support of the PIER program and other funders, has begun to work to create a series of tools that improve the applicability of SDM modeling for conservation and management applications. That work is extended here, looking to better address fine-scale climates experienced by individual plants or small groups of plants, integrate results across hundreds or thousands of species, and to better incorporate dynamics associated with species competition and disturbance, particularly fire.

The work under this project focuses on three broad areas of improved tools for land use and conservation planning of biological systems under climate change. First is refinement of scale of analysis, to permit biological simulations that resolve topography, soils and other features within a typical land use management area, park or reserve. The second is the improvement of a conservation planning tool for climate change that can be applied to large numbers of species and large areas (California or the Western U.S.). The third tool is further improvement of the BioMove model developed in previous grants. A brief history of each of these tools and their importance is presented below.

#### 1.1.1 Fine-Scale Modeling

Fine-scale modeling has been a goal in research into biological responses to climate change for at least two decades. However, while biological research has tended to use relatively fine-scale climatologies relative to GCM simulations that are typically hundreds of kilometers in horizontal resolution, the 10-50km or coarser modeling typical of the biological change literature of twenty years ago is still very coarse relative to important biological scales.

Plants respond to climate at the level of the individual. It is the survival of individual plants that determines a species' range boundary, or its movement under climate change. Further, it is increasingly acknowledged that small patches of forest have played a critical role in vegetation responses to rapid climate change emerging from the last glacial period. Since human-induced climate change is likely to be as fast as or faster than the fastest regional climate change in the past 20,000 years, understanding the conditions that govern existence of small patches of vegetation are critical to understanding the future impacts of climate change.

Fortunately, over the past decade, two trends have facilitated biological modeling at finer scales. First, climate model resolutions are continually improving. GCM resolution is becoming finer, and within five years most GCMs will have horizontal resolutions of 100km or less – a 5 or 10-fold improvement in resolution over models of a decade ago. Regional climate models are now being run at scales of 10s of kilometers. The second factor is the increasing emphasis on fine-scale modeling in biology. The WorldClim website in particular has offered future climate scenarios at scales of 5km and 1km for multiple GCMs and emissions scenarios.

The next breakthrough in scale came from the collaboration of biologists with physical scientists or biologists employing climate downscaling techniques borrowed from the physical sciences. A handful of biological research groups worldwide have begun to experiment with climate

downscales at resolutions of tens of meters – fine enough in scale to capture the micro-climates affecting small patches of forest or vegetation, if not the conditions impacting individual plants.

The fine-scale working group supported under this grant is one of these fine-scale modeling efforts. It is one of no more than five such efforts worldwide that are pioneering this research. The group is probably the best example of integration of biological and physical scientists, in contrast to other efforts that have involved a single physical scientist working with biologists or biologists implementing physical science tools, this group has broad representation from the physical and natural sciences, including 4 physical scientists (climatologists and hydrologists), 6 natural scientists and 2 conservationists.

#### 1.1.2 Conservation Planning – Network Flow

Network Flow analysis is a conservation planning tool for climate change that arose from a working group modeled on NCEAS (National Center for Ecological Analysis and Synthesis, UCSB) methods that was led by the PI of this grant and organized by Conservation International, NCEAS and UCSB. Participants in the 'Conservation Planning for Climate Change' working group included Sandy Andelman (previously Assistant Director of NCEAS, currently head of the Tropical Ecosystem Assessment and Monitoring, TEAM network), Miguel Araujo, a leading SDM researcher currently at the University of Madrid, Paul Williams of the Natural History Museum (London) and Guy Midgley of the South Africa National Biodiversity Institute at Kirstenbosch.

The working group tackled the problem of conservation of multiple species all moving simultaneously in response to climate change. The principle data set for the group was a series of models for over 300 species of proteas in the Cape Floristic Region of South Africa. Large multi-species modeling efforts for Mexico and Europe provided additional test data. The group worked primarily in the WorldMap conservation planning software developed by Paul Williams.

The solution for multi-species planning under climate change developed by the group centered around the concept of 'chains' of suitable habitat from the present to the future. If a species is to survive from the present to the future as climate changes, it must have suitable habitat in each time step from the present to the future. Further, that suitable habitat must be connected in a way such that the species, depending on its dispersal capabilities, can reach suitable habitat between each timestep. For instance, a protea which reproduces after fire and can disperse 10km might be expected to disperse 10km or more per decade in a region with a fire return interval of 5 years.

Williams created an algorithm in WorldMap that searched for contiguous habitat between timesteps, constrained by species dispersal capabilities (Williams et al. 2005). The future habitat suitability in a timestep is derived from an SDM for the species generated with climate information from a GCM. Based on this suitability information and information about dispersal capability, the algorithm searches for suitable habitat within a defined radius, identifying 'chains' of suitable habitat through time. In a final step, the algorithm selects planning units that will conserve all species in all timesteps in the least possible area.

This algorithm was improved after a version of the Cape work was presented at a symposium on conservation planning for climate change at the Society for Conservation Biology. Steven Phillips, the creator of MaxEnt attended the session and recognized that the efficiency of the algorithm could be improved by applying commercial optimization software. Phillips then implemented the new method using the Network Flow approach and showed that it resulted in a more efficient (less area required) solution for the Cape proteas, using exactly the same data as Williams had used for the WorldMap algorithm.

This state-of-the-art algorithm for conservation planning for climate change faced significant practical obstacles, however. The Cape planning area is small and most protea species have very restricted ranges and small dispersal distances. This meant that finding a solution for the Cape using Network Flow was not computationally intense (runs taking hours or days). However, for larger areas and species with larger ranges, the problem becomes much more computationally intensive – making it impossible to implement Network Flow for areas such as California without prohibitive computation times (individual runs taking weeks or months).

The project undertook to adapt the Network Flow optimization approach to large areas and large numbers of species. We were able to accomplish this goal for California, meaning that results are available for California and that the Network Flow approach can be applied to conservation planning for climate change problems in other large, species-rich areas.

#### 1.1.3 BioMove Improvements

BioMove is a new-generation, dynamic modeling tool for assessing species responses to climate change developed under previous support from PIER and the California Energy Commission climate change research program. BioMove has many capabilities that introduce dynamism into climate change modeling of species' responses, including modules addressing species dispersal, inter-species competition and disturbance. One element of BioMove particularly relevant to California environments is simulation of fire impacts on species' response to climate change (and, less directly, possible species shift impacts on fire regime).

The project improved fire modeling using BioMove by gathering parameters for fire-sensitive species, simulating fire impacts on additional species and by incorporating data from previous studies of fire in California. These improvements have expanded our understanding of how BioMove can be used to simulate the effects of changing fire frequency on plant responses to climate change. The results of future simulations using these techniques can help conservationists and land use planners understand the effects of climate change on species and ecosystems.

#### 1.2 Project Objectives

The objective of the project were to improve tools for fine-scale modeling of biological impacts of climate change, conservation planning for climate change and dynamic modeling of species to climate change incorporating finer-scale climatologies and disturbance (especially fire). To achieve these objectives, the project identified six technical tasks, including timestep modeling, conservation site selection, support for fine-scale modeling, a working group on fine-scale modeling and improvement of BioMove simulation of fire impacts. Together with reporting

and outreach tasks, these six technical tasks allowed substantial progress in developing tools useful for conservationists and land use planners interested in the effects of climate change on natural vegetation in California.

Two of the technical tasks (timestep modeling and site selection) combine to produce the improvements that allow application of the Network Flow approach in large, species-rich areas such as California. Two other technical tasks (fine-scale modeling and working group) contributed to better modeling tools for fine-scale simulations, while the final technical task produced improved BioMove simulation capability for fire and fine-scale modeling. Our three non-technical tasks were project administration, data transfer and this final report.

#### 1.3 Report Organization

The remainder of this report consists of 3 sections, corresponding to the three main contributions of the project – fine-scale modeling, Network Flow and BioMove fire and fine-scale simulations. Section 2 provides a description of our results from fine-scale modeling activities. Section 3 outlines the methods and results of our application of Network Flow to the large area, species-rich case of California. Section 4 describes examples of BioMove simulations using improved fire and fine-scale methods. We conclude with a summary of the findings from this work and recommendations for future research.

Each section begins with an overview of the problem addressed, then describes methods developed to address the problem and then concludes with the results of the new method or examples of implementation of the new tools. Because of the dynamic nature of the tools involved, we illustrate each section with final products and screenshots of model runs in progress. Links to online dynamic examples are given. Data compiled by the project, species models using fine-scale climatologies and in decadal timesteps for Network Flow analysis and training materials are available for public download at the website biogeog.bren.ucsb.

#### **CHAPTER 2:**

## Decadal Modeling of California Native Plant Species – Conservation Prioritization Using Network Flow

#### 2.1 Introduction

The continued conservation of native species and the preservation of healthy, functioning ecosystems of the Western US is a difficult and complex exercise that faces multiple threats in the coming decades. It has been demonstrated that 20<sup>th</sup> century climate change has already exerted influence over species ranges and altered community composition (Moritz, Parmesan etc.) Projected climate change through the end of the century will likely result in a geographic redistribution of the suitable climatic habitat for a given species and will create extinction risk for many narrowly distributed or dispersal limited species (Ackerly et al. 2008, Hannah et al. 2012).

Species also face risk of habitat loss and fragmentation as a result of exurban housing growth, conversion to agricultural lands, or expanded natural resource development. This effect is best recognized as the steady encroachment of human influence on previously undeveloped land or designated wilderness areas (e.g. Radeloff et al. 2010) with population growth and demand for low-density housing with a natural aesthetic as drivers of the expansion. However, increased development of traditional or renewable energy resources – along with the associated the infrastructure (e.g. transmission corridors, access roads) -- on federal lands will potentially disturb landscapes that are far removed from any population center. In the case of renewable energy development, the installation of new generation facilities is at least partially driven by a motivation to reduce CO<sub>2</sub> output to mitigate the potentially damaging effects of climate change and thus creates a trade-off tension with strict land conservation to achieve the common goal of conserving species in the face of climate change.

The effects of habitat loss and fragmentation are well-recognized (e.g. Krauss et al. 2010) and there are several commonly used tools to optimize a reserve selection to meet a defined conservation objective at minimum cost (e.g. Marxan; Watts et al. 2009). The difficulty that arises for conservation planners under climate change is that suitable climate space for species shifts through time, while species' abilities to disperse may not be compatible with the velocity of shifting climates on the landscape (Loarie et al. 2009). Traditional conservation instruments, ranging from strict reserves to conservation easements, are static and are not positioned with changing climate and shifting species ranges in mind (Hannah 2005). There is now a clear need for conservation planning tools that will allow identification and prioritization of protected areas that will be able to support species movements in response to climate change (Shaw et al. 2012).

A majority of existing methods used to identify potentially important areas for conservation are not optimized to dynamically respond to climate change impacts on species distribution or projections of economic development. Previous studies have employed species distribution models to project species ranges under climate change to generate optimal reserve designs in

several time steps, and then identify areas that are either overlapping or contiguous across time (e.g Rayfield et al. 2008). Zonation software (Moilanen 2005) represents a refinement of this approach that prioritizes areas that will help facilitate the dispersal of species among reserves in successive time steps has been demonstrated across multiple taxa in Madagascar (Kremen et al. 2008), the Pacific Northwest (Carrol et al. 2010), and for offshore marine protected areas (Leathwick et al. 2008). Although Zonation is a powerful tool for conservation priority setting under climate change, its application thus far has failed to explicitly account for dispersal constrained protection in the intermediary time steps between the end points of 'current climate' and 'future climate'.

As a means of identifying the optimal areas that are needed to ensure the continued protection of thousands of native California plan species under 21<sup>st</sup> century climate change, we applied Network Flow Analysis (NFA) across the statewide domain. The NFA presented here is constructed as described in Phillips et al. 2008, but implemented in a widely available optimization software package, Gurobi Optimizer version 4.5 (Gurobi 2011).

The NFA optimizes spatial sharing of connected conservation parcels required to meet a specified minimum conserved area for all modeled plant species over the analytical time period. The resultant outputs represent the specific areas required to ensure spatial and temporal connectivity of suitable habitat through time, constrained by assumptions of a species ability to disperse. Essential connectivity chains identified by NFA that are not currently within either protected areas or developed lands represent potential focal areas for conservation action to adapt the state's conservation portfolio to projected climate change. The NFA output can also be queried to establish species lists for any defined focal areas or to show the chains formed by individual species. As an example, Figure 2.9 depicts the required chains of Purple Sage (*Salvia leucophylla*), which are modeled to be concentrated in Santa Barbara and Ventura counties.

In conducting this analysis, we have identified focal regions that are vital in maintaining dispersal-connected suitable climate space through 2080 for all species across multiple GCMs and dispersal assumptions. We have also identified regions for a subset of 34 species that are rare within California that are only able to minimally achieve the predetermined conservation area targets – and are therefore of particular importance in establishing statewide priorities for spatio-temporal connectivity for sensitive species. Finally, we were able to determine which species are not able to achieve the conservation targets and are therefore particularly vulnerable to projected climate change.

In addition to conducting the optimization and site selection analysis presented in this report, we have developed a software package that will allow users to implement NFA in R (freely available to all users) and Gurobi optimization software (available through commercial, personal, or free academic license). The cpnf (Conservation Prioritization Using Network Flow) package was developed and is maintained by Oliver Soong (UC Santa Barbara) and may be obtained at http://www.bren.ucsb.edu/~osoong/cpnf\_0.6-16.zip. Successful and efficient implementation of NFA through the cpnf package will likely require some experience in common species distribution modeling tools (e.g. Maxent, GLM, BIOMOD) as well as basic R commands. The full documentation with code examples and sample dataset is included within

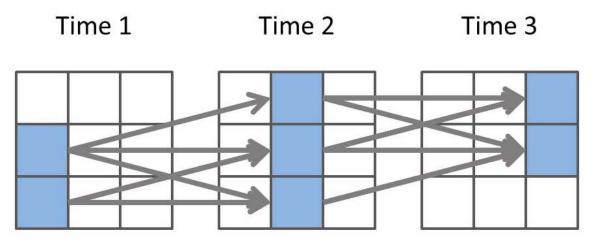
the package download and is presented here in Appendix A. A brief tutorial for users who are less experienced with R, including step by step instructions and sample code snippets, will be available for download along with the 'R' package.

#### 2.2 Methods

In NFA, the modeled range of a single species through time is treated as a directed network, with nodes representing pixels of suitable habitat and edges connecting nodes at one time step with nodes in the next time step that are within a defined dispersal range. A connectivity chain is formed by a continuous path or a set of pixels in which a species can disperse from currently suitable habitat through all time steps to future suitable habitat (Figure 2.1).

Figure 2.1: Schematic Diagram of a Dispersal-Connected Chain of Suitable Habitat.

Regions shaded blue represent suitable habitat in each time step on a 3 x 3 grid. Grey arrows represent possible chains within a species dispersal capability necessary to retain suitable habitat in all time steps.



We conducted our analysis with modeled ranges of 2,235 native California plant species at ~4 km grid cell resolution. This relatively coarse resolution was necessary to solve the problem for all species over the statewide domain within a reasonable timeframe to test and refine the methodology. Distribution models for native species (as designated by Calflora 2009) with >10 pixels containing known occurrences were generated for each decadal time step in Maxent. We utilized species distribution maps at decadal time steps based on two climate model outputs (PCM and GFDL under the A2 emissions scenario), two time periods (2000–2050 and 2000–2080).

To limit the size of the optimization problem, we pre-screened and excluded all species that were able to satisfy their required number of chains using existing protected areas alone. Then we iteratively performed multiple optimizations, beginning with a few rare species, and gradually added more common species, checking at each step which species satisfied their requirements with the current solution and included only those that did not. Due to considerations of computational resources and time, (problems involving thousands of species over the statewide domain would often take 2-3 weeks to run) we terminated the optimizations

early such that our solutions were not guaranteed to be globally optimal, but were within some quantifiable error from the true global optimum.

We conducted NFA for two minimum areas of suitable habitat requirements for all species in each time step (100 and 1000 square kilometers [km²]) and three dispersal radii (0, 6.3, and 10.5 km/time step). The 100 km² target is an International Union for Conservation of Nature (IUCN) threshold for species endangerment. The 1,000 km² target is an arbitrary order-of-magnitude increase in that target, is useful for visualization of important regions for statewide temporal connectivity, and can be conceptualized as 10-fold redundancy of the IUCN threshold target. The three dispersal assumptions that were modeled included no dispersal, limited dispersal of 1.5 grid cells (the 8-neighbor rule), and intermediate dispersal of 2.5 grid cells (the 25-neighbor rule). Dispersal assumptions were universally applied across all species in a scenario.

GFDL,d=1.5,t=2080,r=57

existing protection
developed
additional protection
all chains
Salvia leucophylia

Figure 2.2: Example Chains for All Species (Red Lines) and an Individual Species, Salvia Leucophylla (Blue Lines).

Areas that are classified as developed in the National Land Cover Dataset 2001 (Homer et al. 2004) were considered as never suitable for any species, and were thus excluded from forming

chains of suitability in this analysis. We defined existing protected areas as pixels comprising more than two-thirds of protected areas with a GAP¹ status of 1 or 2, in either the Conservation Biology Institute or the USGS version of the Protected Areas Database (CBI 2010; USGS 2011). These existing protection pixels are considered protected in perpetuity (i.e., chains can use these pixels without increasing the number of additional protected pixels needed).

To identify potential priority areas for spatio-temporal connectivity, we employed two methods. First we highlighted pixels that were selected for additional protection under both the 100 km² and the 1,000 km² suitable habitat requirements. Second, we identified chains that were essential to the solution across all model scenarios. Identifying clusters of grid cells that are selected for additional protection and that comprise required connectivity chains across all GCMs and dispersal assumption reveals focal regions that are consistently important to ensure continued connectivity and are currently unprotected.

Through the initial analysis that incorporated all native California plant species for which sufficient occurrence data was available, we were able to differentiate between species that, by virtue of broad distribution, diverse climate tolerance, or proximity to existing protected areas, are easily able to achieve the conservation area targets from those that are only able to minimally achieve the targets. This latter group of vulnerable species contributes disproportionately to the statewide optimization solutions and is a primary driver of determining which areas are selected for additional protection. To conduct an optimization for additional protection that further prioritizes focal regions based on the connectivity requirements of comparatively uncommon and narrowly distributed species, we cross-walked the group of species that are able to minimally achieve conservation area targets with species that are classified as 'rare' by the California Native Plant Society state ranking system. The resulting 34 species (see Table 2.1 and Section 2.3.2) are primarily herbaceous plants that are endemic to California and represent a diverse sample of California's ecoregions.

#### 2.3 Results

#### 2.3.1 Optimization for 2,235 Native Plant Species

Nearly 70 percent of modeled species were able to form connectivity chains within existing protected areas. Additionally, roughly 5 percent of species were not able to form the minimum required number of chains under any future climate scenario or dispersal assumption (see Table 2.1). As expected, greater assumed dispersal distance resulted in fewer species that were not able to attain suitable habitat requirements in all time steps. Additionally, models with PCM climate data, which shows less dramatic temperature increases and greater precipitation than GFDL within California, allows for more species to attain suitable habitat requirements.

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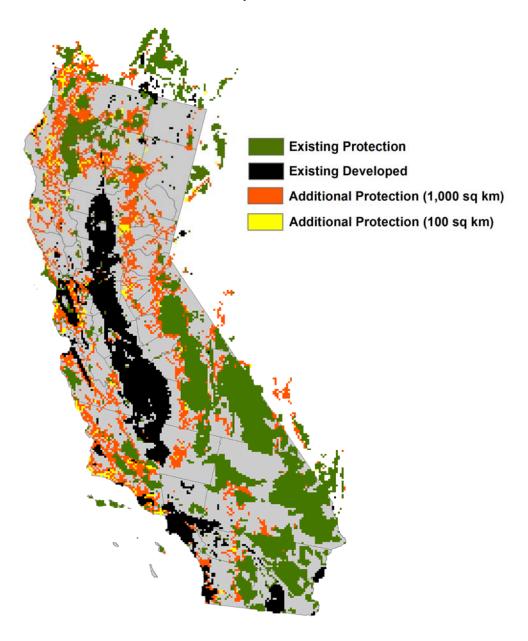
<sup>&</sup>lt;sup>1</sup> U.S. Geological Survey, Gap Analysis Program (GAP).

Table 2.1: Species That Are Unable to Achieve Minimum Conservation Area Targets under Any GCM or Dispersal Scenario.

Abies amabilis	Cronic bakari	Minuartia rosei
	Crepis bakeri Cuscuta denticulata	Minuartia rubella
Abies lasiocarpa  Acanthomintha obovata	Cuscuta dell'ilculata  Cuscuta salina	
		Mirabilis multiflora
Achnatherum nevadense	Cycladenia humilis	Mitella caulescens
Allium atrorubens	Delphinium andersonii	Monanthochloe littoralis
Allium burlewii	Draba breweri	Monolopia lanceolata
Anemone multifida	Draba densifolia	Monolopia stricta
Anulocaulis annulatus	Epilobium siskiyouense	Nassella cernua
Aquilegia eximia	Eriastrum pluriflorum	Navarretia breweri
Aquilegia pubescens	Eriastrum wilcoxii	Navarretia prostrata
Arabis rigidissima	Ericameria discoidea	Nothochelone nemorosa
Arctostaphylos bakeri	Ericameria nana	Palafoxia arida
Arctostaphylos klamathensis	Ericameria ophitidis	Pedicularis howellii
Arnica longifolia	Erigeron aliceae	Phacelia ciliata
Astragalus didymocarpus	Eriodictyon tomentosum	Phacelia crenulata
Atriplex spinifera	Eriogonum davidsonii	Phlox stansburyi
Batis maritima	Eriogonum giganteum	Phyllodoce empetriformis
Botrychium minganense	Eriogonum hirtellum	Picea engelmannii
Bouteloua eriopoda	Eriogonum microthecum	Pinus washoensis
Brodiaea appendiculata	Galium clementis	Poa piperi
Calamagrostis rubescens	Galium hypotrichium	Polystichum lemmonii
Calochortus macrocarpus	Galium multiflorum	Populus balsamifera
Calyptridium pygmaeum	Gentiana plurisetosa	Primula suffrutescens
Camissonia brevipes	Geraea canescens	Salix arctica
Camissonia tanacetifolia	Geum triflorum	Salix breweri
Carex echinata	Hackelia amethystina	Salix sitchensis
Carex fissuricola	Hesperostipa comata	Sambucus melanocarpa
Carex interior	Hulsea algida	Saxifraga odontoloma
Carex praeceptorum	Ivesia pygmaea	Sedum oregonense
Carex tahoensis	Juncus bolanderi	Sidalcea reptans
Castilleja parviflora	Juncus howellii	Silene bernardina
Ceanothus roderickii	Lasthenia fremontii	Silene menziesii
Chaenactis alpigena	Lewisia leana	Solidago guiradonis
Chamaesyce micromera	Leymus cinereus	Suaeda californica
Chamaesyce parishii	Lilium columbianum	Systenotheca vortriedei
Chamaesyce revoluta	Limonium californicum	Tetracoccus hallii
Chamaesyce setiloba	Linum lewisii	Tetradymia argyraea
Chenopodium fremontii	Lomatium congdonii	Tidestromia oblongifolia
Chorizanthe cuspidata	Luetkea pectinata	
Chorizanthe xanti	Lupinus gracilentus	
Chrysothamnus greenei	Lupinus obtusilobus	
Cinna latifolia	Lupinus tracyi	
Clarkia borealis	Mentzelia congesta	
	Mimulus lewisii	
Coreopsis stillmanii	iviimulus iewisii	

Species that are able to form chains and meet the suitable habitat requirement in areas that are outside of existing protection account for the "additional protection" results. The Figures 2.3 and 2.4 below represent the NFA results under the A2 emissions scenario driven by the GFDL GCM . In each figure, two targets for connectivity are represented, 1,000 km² (orange) and 100 km² (yellow). Nearly all of the pixels selected for the  $100 \text{ km}^2$  solution are also included in the  $1,000 \text{km}^2$  solution. Pixels in yellow can therefore be interpreted as part of both target conservation area solutions.

Figure 2.3: Sites Selected for Additional Protection through 2080 for 1,000 sq km (Orange) and 100 sq km (Yellow) Conservation Area Targets. GFDL Model; A2 Emissions Scenario; 0.6 km/yr Dispersal.



Broad areas in several parts of the state are highlighted in orange and yellow, indicating that they are conservation priorities to maintain connectivity for plants as climate changes (Figures 2.3 and 2.4). Land tenure in these priority areas may be private or public. On public multipleuse lands, zonation for biodiversity protection in these priority areas may be appropriate. Private lands may be conserved with conservation easements or through acquisition.

Although the specific pixels selected for additional protection varied according to GCM and dispersal assumption, but certain regions were consistently selected in each simulation. First, many areas are adjacent to existing protected areas, as the algorithm by virtue of the cost surfaces that were included in the optimization preferentially selects areas that can make use of connectivity within existing protected areas (zero cost). Second, it is evident that the elevational gradient that surrounds the Central Valley is important for statewide climatic connectivity as these corridors will allow lower elevation foothill or valley species to move into protected areas of comparatively higher elevation as climatic suitabilities shift upslope. Third, though less pronounced, several areas that exploit coastward temperature gradients emerge as important connectivity areas (e.g. south coast of Santa Barbara County, Monterrey Peninsula, and coastal Marin County). Finally, undeveloped areas that surround major urban centers are important areas for additional protection. This is especially evident in the areas surrounding the San Francisco Bay Area and in the undeveloped areas east of San Diego.

Not all species are able to achieve enough chains to meet the suitable habitat target. The areas which do harbor these species in all time steps represent potential core areas of temporal connectivity. Chains formed by these species are represented in Figure 2.5. They are "required chains" in the sense that because the species fails to meet the habitat suitability target, anywhere the species *does* have a chain is required in the conservation solution. Stacking the chains required to meet the minimum area target for all species in all model simulations reveals focal areas that deserve consideration for future conservation.

Figure 2.4: Sites Selected for Additional Protection through 2080 for 1,000 sq km (Orange) and 100 sq km (Yellow) Conservation Area Targets. GFDL Model; A2 Emissions Scenario; 1.0 km/yr Dispersal.

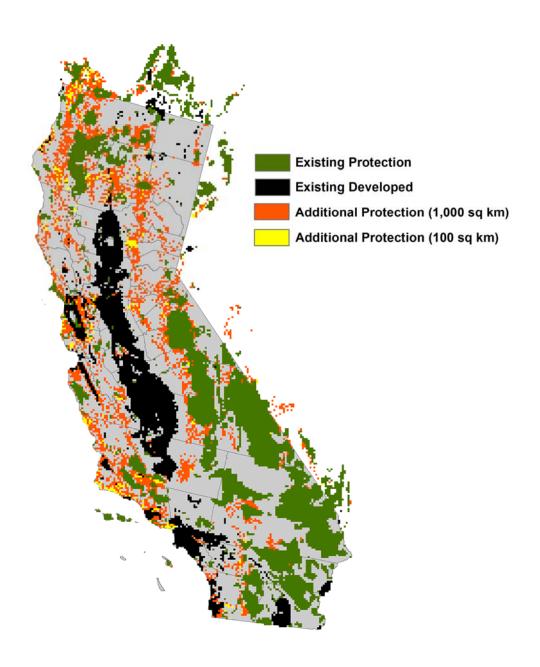
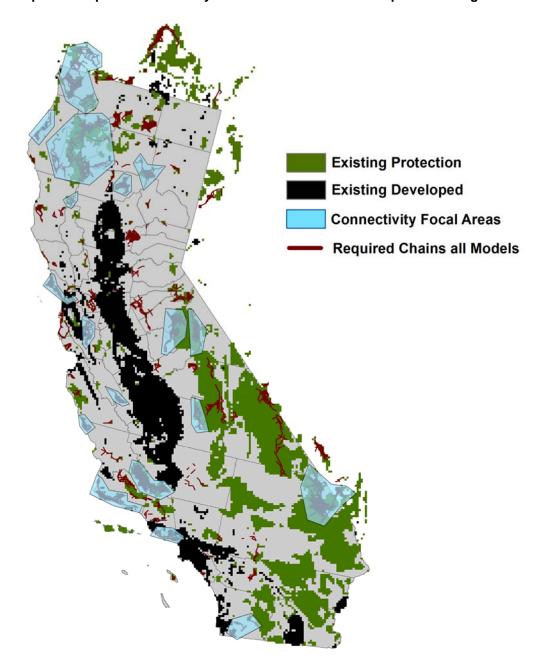


Figure 2.5: Required Connectivity Chains for All Models (Red Lines) and Focal Areas Important for Spatio-Temporal Connectivity for Native California Plant Species through 2080.



Many of the focal areas depicted in Figure 2.5 are either entirely within or, more importantly, adjacent to existing protected areas. This emphasizes the importance of leveraging or possibly expanding the state's current portfolio of GAP status 1 or 2 protected areas. Prominent protected areas that are at the center of a focal region include: Mojave National Reserve, Sequoia/King's Canyon National Park, Yosemite National Park, Trinity National Forest, Pt. Reyes National Seashore, Lassen National Park and Carrizo Plain National Monument. Furthermore, additional focal area are anchored by conservation holdings that are not classified as GAP status 1 or 2 such as the Santa Monica Mountains National Recreation Area, the Mount

Hamilton region south and east of the San Francisco Bay Area and the south coast of Santa Barbara county. All three of the focal areas are near extensive populated areas and are therefore at heightened risk of further fragmentation or development in the coming decades.

#### 2.3.2 Optimization for 34 Rare Plant Species

From the optimization of all available native California plant species, we were able to determine which species were only minimally achieve the 100km2 conservation target in all timesteps (species that comprise the "required chains" above). To conduct an optimization that focuses on rare and potentially vulnerable species, we selected a subset of species that form "required chains" and are also classified as rare by the California Native Plant Society's rare plant inventory state ranking system. This subset of species is listed in Table 2.2.

Optimization results for this comparatively narrow subset of species are, as expected, less broadly dispersed. Figures 2.6 and 2.7 depict the areas selected for additional protection under the more restrictive (hotter and drier) GFDL climate scenario for 0.6 km/yr and 1 km/yr dispersal respectively. Several unique areas, often specific to an individual species, are highlighted as essential corridors for continued conservation under climate change. A section of the transverse range from western Santa Barbara County to the undeveloped areas that surround Ventura is selected under both dispersal assumptions. This selected area is due primarily to the chains formed *by Juglans californica, Calystegia collina venusta*, and *Chorizanthe breweri*. Similarly, an area of the Temblor range that straddles southern San Benito county and western Fresno county is also due to the required chains of *Calystegia collina venusta* as well as *Navaretia prostrata*. A striking corridor that exploits an elevational gradient from the areas between Red Bluff and Redding to Trinity National Forest supports the connected suitable climate range of *Delphinium variegatum*. Finally, selected areas of the San Francisco Bay peninsula and the Santa Cruz Mountains are important for several species including *Delphinium variegata*, *Campanula californica*, and *Ribies menzii*.

Table 2.2: Subset of Rare CA Plant Species Used for 34 Species NFA Optimization.

Species	Common Name	Rare Plant Rank	State Rank	CA Endemic
Astragalus didymocarpus	Miles' milk-vetch	1B.2	S2.2	Т
Astragalus kentrophyta danaus	Sweetwater Mountains milk- vetch	4.3	S3	Т
Blennosperma nanum nanum	Point Reyes blennosperma	1B.2	S2	Т
Bouteloua eriopoda	black grama	4.2	S3.2	F
Calystegia collina venusta	South Coast Range morning- glory	4.3	S3.2	Т
Calystegia subacaulis subacaulis	Cambria morning-glory	4.2	S3	Т
Campanula californica	swamp harebell	1B.2	S3	Т
Chaenactis glabriuscula orcuttiana	Orcutt's pincushion	1B.1	S1	F
Chlorogalum grandiflorum	Red Hills soaproot	1B.2	S3	Т
Chorizanthe breweri	Brewer's spineflower	1B.3	S2.2	Т
Chorizanthe xanti	white-bracted spineflower	1B.2	S2	Т
Clarkia biloba brandegeae	Brandegee's clarkia	1B.2	S3	Т
Delphinium variegatum	Thorne's royal larkspur	1B.1	S2	Т
Ericameria ophitidis	serpentine goldenbush	4.3	S3.3	Т
Erigeron petrophilus sierrensis	northern Sierra daisy	4.3	S3.3	Т
Eriogonum crocatum	conejo buckwheat	1B.2	S2.1	Т
Eriogonum nudum indictum	protruding buckwheat	4.2	S3.2	Т
Eriogonum tripodum	tripod buckwheat	4.2	S3.2	Т
Githopsis pulchella serpentinicola	serpentine bluecup	4.3	S3.3	Т
Hackelia amethystina	amethyst stickseed	4.3	S3.3	Т
Hesperolinon breweri	Brewer's western flax	1B.2	S2	Т
Hesperolinon tehamense	Tehama County western flax	1B.3	S2	Т
Hibiscus lasiocarpus	woolly rose-mallow	1B.2	S2.2	Т
Holocarpha virgate elongata	graceful tarplant	4.2	S3.2	Т
Juglans californica	Southern California black walnut	4.2	S3.2	Т
Layia munzii	Munz's tidy-tips	1B.2	S1.1	Т
Lepechinia fragrans	fragrant pitcher sage	4.2	S3.2	Т
Monardella antonina benitensis	San Benito monardella	4.3	S3.3	Т
Navarretia prostrata	prostrate vernal pool navarretia	1B.1	S2	Т
Phacelia ciliata	Merced phacelia	1B.2	S1.2	Т
Podistera nevadensis	Sierra podistera	4.3	S3.3	Т
Ribes menziesii	aromatic canyon gooseberry	1B.2	S2.2	Т
Viguiera laciniata	San Diego County viguiera	4.2	S3.2	F
Wyethia reticulata	El Dorado County mule ears	1B.2	S2	Т

Figure 2.6: Sites Selected for Additional Protection (34 Rare Species Subset) through 2080 for 1,000 sq km (Orange) and 100 sq km (Yellow) Conservation Area Targets. GFDL Model; A2 Emissions Scenario; 0.6 km/yr Dispersal.

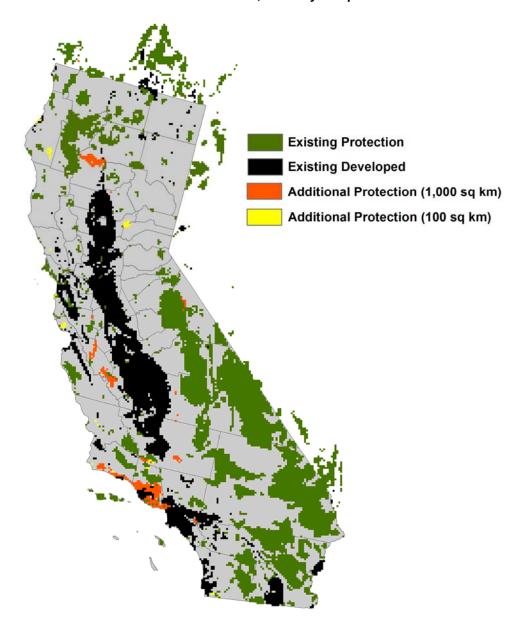


Figure 2.7: Sites Selected for Additional Protection (34 Rare Species Subset) through 2080 for 1,000 sq km (Orange) and 100 sq km (Yellow) Conservation Area Targets. GFDL Model; A2 Emissions Scenario; 1.0 km/yr Dispersal.

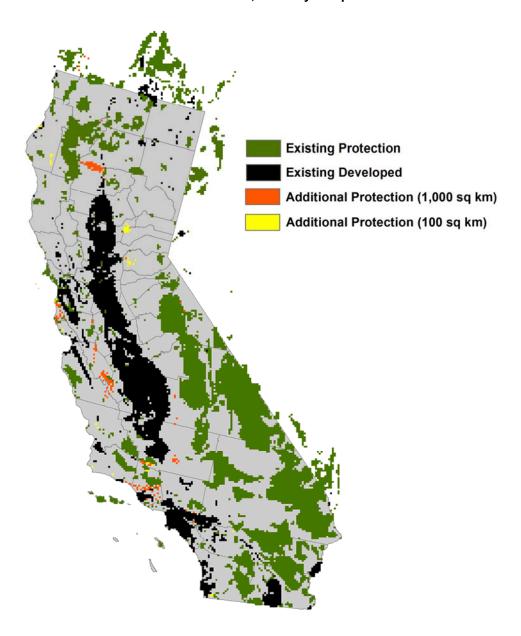
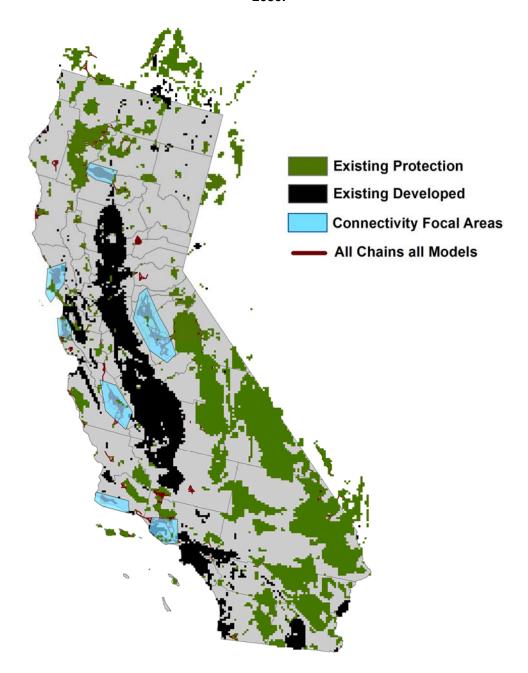


Figure 2.8: Required Connectivity Chains for All Models (Red Lines) and Focal Areas Important for Spatio-Temporal Connectivity for 34 Rare and Range Limited California Plant Species through 2080.



Through the similar approach used with the 2,235 species optimization, we identified focal areas for the rare species subset by selecting dense clusters of connectivity chains. Unlike the full species optimization which only looked at "required chains", the rare species subset focal areas are comprised of all chains formed by the 34 species in each GCM, dispersal, and conservation target iteration. Figure 2.8 shows all chains formed by the 34 species subset as red

lines overlaid by focal areas drawn in blue. The region stretching from the south coast of Santa Barbara county through the Santa Monica Mountains again features prominently in providing dispersal connected suitable habitat for multiple species through the end of the century. Additionally, the natural lands surrounding the San Francisco Bay Area again emerge as focal connectivity areas. These focal areas that are redundant between the full species optimization and the rare species subset are further emphasized as potential priority regions for optimal conservation investment. Subsequent analysis at finer scales within these focal regions, with selected target species of conservation concern, and with more sophisticated cost surfaces could serve to further prioritize specific parcels that are of optimal conservation benefit under climate change.

#### 2.4 Conclusions and Future Research Directions

The results presented here are a successful demonstration of NFA to identify regions that are important for spatio-temporal connectivity of suitable habitat under climate change for a large number of species and a spatial domain the size of California. However, successful testing and implementation of the methodology involved several simplifying assumptions that require careful interpretation of the results. Relatively coarse grid sizes (~4 km) were required to optimize the solution for the entire species dataset at a statewide modeling domain. SDM at such resolution will not accurately represent all the processes that control habitat suitability at the scale of an individual or local population and therefore may omit areas that are climatically suitable that are smaller than the spatial extent of the grid cell, but which are large enough to support viable, persistent populations. This scale effect is potentially a greater issue for narrowly distributed species or species with restricted climate envelopes. The implementation of NFA at finer resolutions, over smaller spatial domains and carefully chosen target species with individually tailored SDM is an important next step in a prioritization exercise. The most recently updated CPNF 'R' package is able to interpreted continuous values of habitat suitability (as opposed to binary presence vs. absence)

The optimization results presented here also rely upon universal assumptions of viable dispersal distance among all species. Clearly, species vary in their capacity to effectively disperse—and viable dispersal distances for an individual species will vary across different landscapes. Refinements to the R package have been made to allow a dispersal distance to be defined for each species in the optimization. Assembling a target species list with thoroughly vetted individual dispersal distances is an important research priority moving forward.

With the flexibility of optimization implementation afforded by the CPNF 'R' package, there is a great opportunity to prioritize conservation site selection with more complexity and sophistication given to the cost surfaces. As described, the optimization results presented here simply treat cost as a binary between protected areas (zero cost) and non-protected areas (cost of one per pixel). The 'R' package is able to accept any number of cost surfaces, keeping in mind that each additional cost surface increases the size of the optimization problem. However, optimizations conducted over limited spatial domains with carefully chosen species list could be implemented with cost surfaces that account for varying levels of protection, existing housing/population density, vulnerability to development (via urban growth models e.g.

UPLAN), or actual cost of land acquisition. The incorporation of these additional cost surfaces would add richness to the optimization solutions and make valuable contributions conservation planning and land use decisions. It is our hope that the freely available CPNF 'R' package will allow research to experiment with incorporating such refinements to the analysis presented in this report.

## CHAPTER 3: Modeling Species Distributions with Finescale Climate Data

#### 3.1 Introduction

The working group "Fine-Scale Climate Modeling of Species Responses to Climate Change" (hereafter: 'Fine-scale Group") is an NCEAS working group jointly supported by this grant and funding from the National Science Foundation and the Nature Conservancy. Group participants include biologists from 4 California universities and climatologists from Universities and research institutes. Dan Cayan (Scripps), Kelly Redmond (Desert Research Institute) and Alex Hall (UCLA) were the initial climatologists involved. Biological modelers included Frank Davis (UCSB), Janet Franklin (SDSU, now ASU) and Helen Regen (UC Riverside). Rebecca Shaw (the Nature Conservancy, now Environmental Defense Fund) and Lee Hannah (Conservation International/UCSB) represented conservation NGOs.

The Fine-scale Group began as a meeting of biologists and climatologists at NCEAS (UCSB) to develop fine-scale climatologies for use in biological modeling. The group expanded after its initial meeting to include Alan and Lorrie Flint of USGS, who were actively pursuing the production of fine-scale climatologies and water balance (climatic water deficit) models.

In 2010, the group was awarded a major National Science Foundation (NSF) grant from the Macrosystems Biology program. This \$3.7 million dollar grant was made possible directly because of the groundwork provided by the working group meetings supported by this grant and a grant from The Nature Conservancy to NCEAS. The NSF funding permits high leveraging of the funds from this project, and allows the working group to expand its work to include experimental manipulations and recording of micro-climates in the field.

The group has laid the theoretical foundation for understanding the effect of scale on estimates of species' distributions and their response to climate change (Franklin *et al.* 2012, Seo *et al.* 2009). Among the products of the group and project-supported researchers are examinations of the effects of scale on models species distributions at meso- to coarse-scale (Seo *et a.l.* 2009) and assessment of the effect of scale on outcomes of climate change assessments using species distribution models (Franklin *et al.* 2012). These products were produced with early versions or fore-runners of the climate and water balance downscaling being produced for the working group.

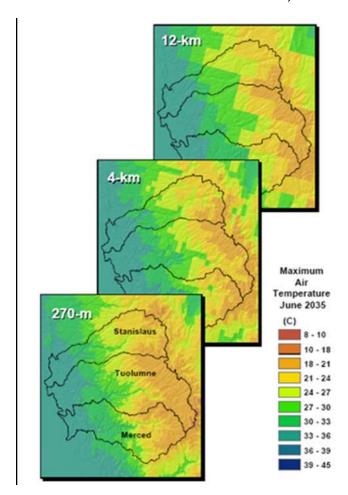


Figure 3.1: Statistical Climate Downscales at 270m, 4km and 12km.

Two types of fine-scale climate models have been developed for the working group analyses. The first is statistically downscaled climatologies and the second is dynamically downscaled climatologies. Statistical downscales are most relevant for temperature and precipitation variables. They use lapse rate and other physical estimators to calculate variable values between measured weather station records. They apply these same approaches to estimating variables at fine scales in future climates. Dynamic downscaling is conducted using Regional Climate Models (RCM). These models are most important for dynamic variables such as wind and fog formation. The scale of statistical downscaling can extend to 90m or finer, while fine-scale dynamic downscaling is limited to scales of 1-2km, still very fine relative to usual RCM scales of 40-60km and usual GCM scales of 80-200km. Thus far, working group analyses have only worked with statistical downscaling.

Seo et al (2009) explored the effects of scale on species distribution modeling and found pronounced effects of scale, including disproportionate increases in simulated range size and decreasing spatial congruence at coarser scales. They found that horizontal resolutions of 4km or less minimized distortions in species with narrow distributions, and 8km for broad range

species. These results suggested that there could be substantial effects of scale in estimates of species range changes or extinction risk due to climate change.

Franklin et al (2012) specifically examined scale effects in climate change assessments using species distribution models (SDM). This is one of the major themes of the working group, and this publication is the first in a series examining scale effects in species models. This study examined scale differences in fine- to medium-scale models, 90m to 4km. The working group is now working with fine scale climatologies down to 30m. Differences found between 90m and 1km or 4km by Franklin et al were less than might have been suggested in the (coarser scale) Seo et al analysis. Differences in range sizes and overlap due to scale were modest, as were scale related differences in projections of stable habitat. However, significant spatial differences did emerge, in different areas for different species. This indicates that scale of modeling may have substantial impact on conservation recommendations generated from species distribution modeling.

The working group is now progressing to finer scale models, as noted above. The finest modeling scale planned is 30m, and 90m may prove to be the finest scale widely applied. For perspective, the finest scale climatologies currently used in most SDM are generally 1km or 800m. A 90m model represents nearly 2 orders of magnitude finer resolution than these typical climatologies and 30m is approximately a 900-fold increase in resolution.

#### 3.2 Methods

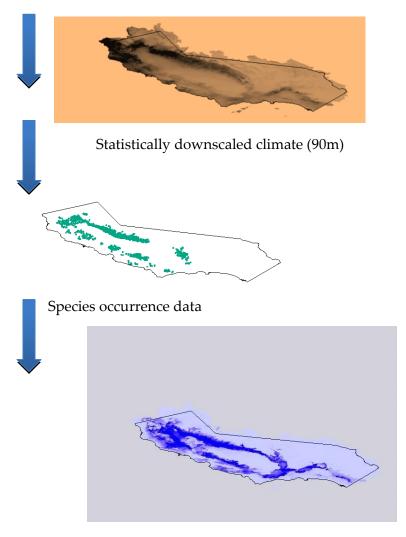
The methods for producing fine-scale climatologies for species distribution modeling include both static (statistical) and dynamic (Regional Climate Model) approaches, as noted above. The fine-scale group will incorporate information from fine-scale (1-2km) Regional Climate Models in the near future, but the results presented in this report will all be derived from statistical downscaling methods.

The schematic illustration of producing an SDM at high resolution is shown in Figure 3.2. First, a coarse climatology from the historical record or a future GCM simulation (GCM simulation in the figure) is statistically downscaled to 90m (or 270m or other fine-scale resolution). The fine-scale climatology and information about the occurrence of the species of interest is then used as input for an SDM. The SDM produces a model of the current or future suitable climate for the species.

Figure 3.2: Steps in Producing a Species Distribution Model with Fine-Scale Climate Data.

First, a coarse-scale climatology from a GCM is statistically downscaled to 90m. That fine-scale climatology is then used with species occurrence data in an SDM to produce a model of the area of suitable climate.

Climate Variable Change from GCM (200km)



Species Distribution Model (SDM)

Species distribution data for each species is assembled from herbarium records, vegetation plots and other geo-referenced records of the plants' occurrence. For fine-scale modeling, the georeferencing has to be accurate at the resolution of the modeling. In general, this means that only modern (post-2001) records geo-referenced by GPS are suitable. In practice, the database of species' occurrences is assembled for all available points, and the records with suitable geo-referencing precision are extracted from the database at the time of modeling. This makes a single species occurrence database useful for modeling at all scales. It does however mean that

the number of records available for fine-scale modeling may be limited. For instance in a species occurrence database, a rare species might have fewer than 1,000 records, but fewer than 100 and perhaps as few as 10-20 that are geo-referenced to within 10m. SDMs generally require 15-20 records to build a reliable model, so less common species may simply have too few high-precision geo-referenced records to build a fine-scale model.

Figure 3.3: Example of Distribution Points for a Species (Aesculus Californicus).

Each green dot represents a species record from a herbarium collection, vegetation plot or Forest Service plot.



Once a present fine-scale model is constructed, that same model is used with input from future climate simulations. Simulations from multiple GCMs and representing multiple emissions pathways will be used, so multiple models are generated for each species. Current and future models are compared, and range lost, range retained and new range are identified (see below). Typical model outputs are identified by future time period (e.g., 2050 or 2100), GCM (e.g., PCM, GFDL, Hadley) and emissions scenario (e.g., A2, B1). Note that GCM simulations using a new emissions pathway system are now appearing (the Representative Concentration Pathways, RCP) but during the work of this grant, the only emissions scenarios available were the SRES (IPCC Special Report on Emissions Scenarios) series.

52 native plant species have been modeled at scales of 90m, 270m, 800m and 4km. The species were selected by working group members to represent narrow, intermediate and broad-ranged species, as well as herbaceous, shrub and tree growth forms. In all, accounting for species, model scale, GCM variants, emissions pathway variants and other factors, over 1,000 models were produced for these species. Models were also produced for one crop species, *Vitis vinifera* – wine grape.

#### 3.3 Results

## 3.3.1 Native Plants

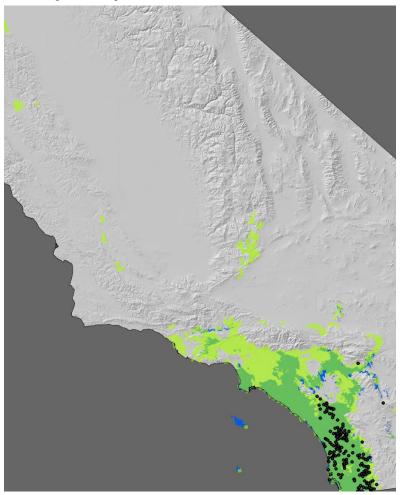
The fine-scale models of the 52 plant species show scale-dependent effects on species modeled range sizes, the degree of overlap of current and future ranges, and across narrow- to broadrange species. The effects on range sizes are not large in most cases and are not statistically significant in many cases (Franklin *et al.* 2012). However, in narrow range species, there is a consistent pattern of coarser scale models projecting larger ranges than fine-scale models, both in the current climate and in future projections.

This effect is illustrated in Figure 3.4. In this example, *Xylococcus bicolor* (Mission manzanita), a narrow range species from Southern California, has modeled range at 4km from the Tehachapis to Mexico. The 90m model projects a much more restricted range, from the Los Angeles basin with outliers near Santa Barbara, to the border. The 90m model matches the known distribution of the species.

The larger ranges estimated with coarser scale models can lead to significant errors in conservation planning. Larger current range equates to a larger range for potential overlap with modeled future range of the species, especially when the over-predicted range is to the north of the known range, as is the case in our example. In cases such as this, northward shifts in suitable climate for the species may appear to overlap with the current range because of the over-prediction, when in fact they would be disjunct from the current range and require significant dispersal (often across heavily urbanized landscapes) to occupy the new range. Conservation plans made using the coarser, over-predicting models might therefore lead to the false conclusion that the species was relatively secure in the face of climate change, thus delaying needed conservation actions.

Figure 3.4: Modeled Range Expands at Coarser Scales.

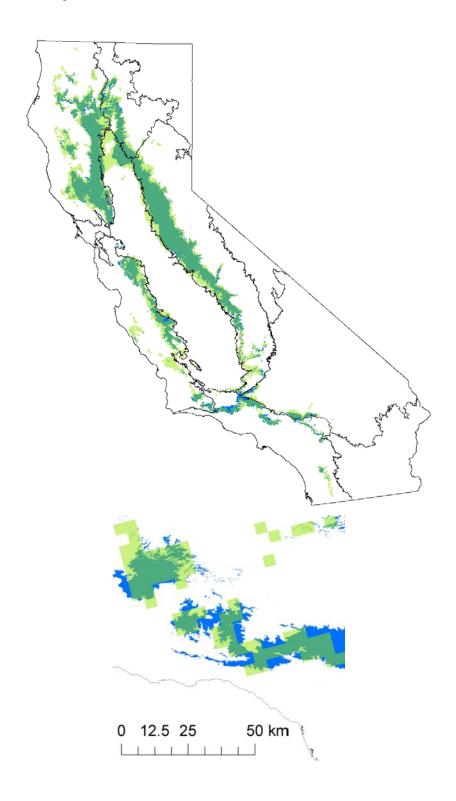
This effect is particularly pronounced for narrow range species. In this example, *Xylococcus bicolor* range is smallest in fine-scale (90m) model, and larger in 4km model. Blue is 90m model only, light green is 4km model only and dark green is agreement between 90m and 4km models.



A second observed pattern in the fine-scale models is geographic disagreement with the coarser-scale models. Even where overall range size and area current and future range overlap are similar in the fine- and coarse-scale models, the location of the range persistence may differ. Figure 3.5 illustrates this using the model of a common pine species, in current climate only. It is apparent that the two models agree substantially on the location and area of suitable range for this species (*Pinus sabiniana*). However, the locational details vary considerably in particular parts of the range. The figure inset illustrates the congruence of the two models of suitability at different scales, in this case the area surrounding Santa Ynez north of Santa Barbara. While models at both scales agree that there is substantial suitable range in this region, the fine-scale model projects some suitable range on hillsides the 4km model does not project as suitable at all.

Figure 3.5: Comparison of Fine-Scale (90m - Blue) and Coarser Scale (4km - Yellow) SDM for Gray Pine (*Pinus Sabiniana*).

The statewide map shows that for much of the range results are congruent. Inset shows that for particular parts of the range, substantial differences exist.



This effect is consistent with differences observed between coarse and fine-scale models in other studies that are emerging in other parts of the world (Trivedi, 2008; Randin 2009).

The significance of these differences is greatly magnified, because effective conservation involves the intersection of remaining natural habitat and protection. Because many protected areas have areas measured in tens of kilometers and remaining natural habitat may sometimes be restricted to patches of tens or hundreds of kilometers, the geographic disagreement between the coarse- and fine-scale models, which itself spans kilometers or tens of kilometers, may be very significant.

For instance, in the example figure, an area of gray pine exists in a narrow band along a hillslope. If this hillslope is forested and within National Forest, it may represent a well-protected population. The coarse (4km) model would miss this population and perhaps bias conservation plans as a result.

As climate change is introduced, the situation becomes even more complex. The task of conserving the species then requires correctly simulating its current distribution relative to remaining habitat and conservation areas, as well as ensuring that populations are conserved in future habitat. In these types of multi-factor, multi-timestep problems, the areas of disagreement between the fine- and coarse-scale models may become very important. The working group is focusing on resolving problems such as these under the ongoing NSF funding.

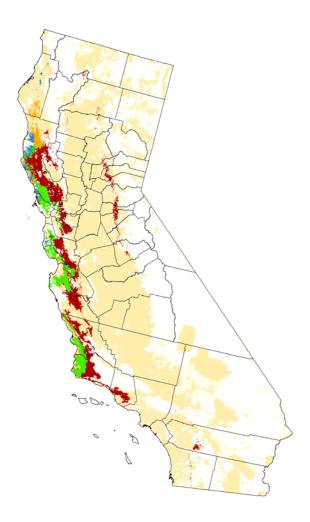
# 3.3.2 Wine Grape Suitability

A novel application of the fine-scale modeling developed by the project but outside of the working group, was the application to a species of agricultural importance, wine grapes (*Vitis vinifera*). Viticultural suitability was chosen because of its economic importance to the state, its sensitivity to climate (especially temperature), and the possible repurcussions on natural habitats of relocation of vineyards.

Figures 3.6 and 3.7 illustrate the fine-scale model results for *Vitis vinifera*. Large areas currently suitable for viticulture are lost by mid-century, with substantial new suitability appearing in many areas, but not enough to balance areas losing suitability. The fine-scale models allow resolution of features such as valleys and hillslopes that provide important micro-climates for vineyards.

Figure 3.6: Fine-Scale (270m) Model of Change in California Wine Grape (*Vitis Vinifera*) Suitability – 2050 GFDL A2.

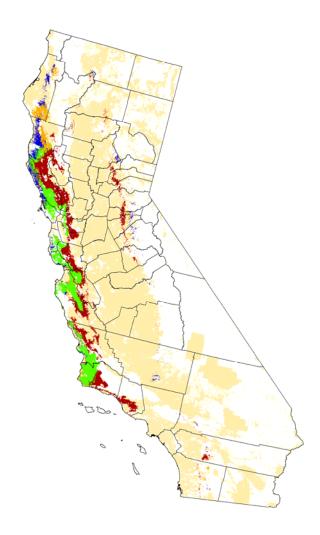
Areas of current suitability that remain suitable in mid-century are shown in green. Areas in which current suitability is lost by 2050 are shown in red, with newly suitable areas in blue.



The difference introduced between GCMs is substantial, but less significant than the agreement on overall patterns of change. The PCM scenario shows more newly suitable area in the Sierras and Northern Coast than does the GFDL scenario. Little wine is grown in the Sierras, so this difference is probably of little significance. More importantly, both GCM variants agree on substantial losses of suitability in current wine-growing regions such as the Napa area. They also agree that coastal growing regions will maintain more suitability than inland areas.

Figure 3.7: Fine-Scale (270m) Model of Change in California Wine Grape (*Vitis Vinifera*) Suitability – 2050 PCM A2.

Areas of current suitability that remain suitable in mid-century are shown in green. Areas in which current suitability is lost by 2050 are shown in red, with newly suitable areas in blue.



Loss of suitability in these models does not mean that wine grape will no longer be grown at a location or that they can no longer be grown. It indicates, rather, declining conditions for growing, highlighting areas in which adaptation measures may be needed. Growers can adapt to temperature changes by trellising vines to increase shading of grape clusters and by switching to varieties that produce well in warmer temperatures. Loss of suitability due to declining rainfall may require irrigation, with serious consequences for water resources management.

The implications for natural systems of this changing viticultural suitability are substantial. Some areas of natural habitat that are not currently suitable for wine grape growing may become suitable, with possible attendant habitat clearing. Water conflicts are of particular concern, both because irrigation needs may increase but also because warmer temperatures may

create incentives for vineyards to use misting to keep grape clusters cool. Water withdrawals for frost control in the Russian River area already cause some streams to run dry when vineyard sprinklers are running. Widespread use of misting could put stress on water resources and native freshwater habitats in many parts of the state.

Advance planning for climate change adaptation in vineyards can help avoid many of these possible negative effects. Models of *Vitis vinifera* suitability help point to areas of priority for adaptation planning that involves both vintners and conservationists. Fine-scale models of suitability help pinpoint areas of particular concern at scales relevant to landscape planning. Even more detailed studies will be needed at the level of individual vineyards, and models such as ours can help point the way to sites in which these detailed studies are most needed. The state can play a beneficial role in facilitating this planning process.

# **CHAPTER 4:**

# Dynamic Species Modeling with BioMove – Incorporation of Finescale Climate Data and Refinements to Fire Module

# 4.1 Introduction

How vegetation in California will respond to climate change is of paramount interest to foresters, land managers, conservation groups, developers and individual land owners. It will also affect the persistence of dependent species thus affecting overall ecosystem health and stability. In California, climate change is likely to result in the poleward and upslope movement of species, effects already seen in other parts of the earth (Parmesan et al. 2006). These effects may be confounded by land use change as California's population continues to grow and place greater demands on its natural resources. It is evident that correlative species distribution models fail to address the dynamic nature of populations and do not account for dispersal constraints, changes in disturbance regimes or species interactions. Regardless of the niche described by climatic and/or soil limitations, a species will not realize a potential niche if limited by certain life history constraints. In order to maintain the biological integrity of California's ecosystems and the services they provide, we must continue to develop better predictive tools for assessing species' response to climate change.

BioMove is an integrated niche and population model that is useful in assessing how species distributions will respond to climate change (Midgley et al. 2010). The model is implemented within the Landscape Modeling Shell (Lamos) software, which allows ready interchange of other model elements, including disturbance dispersal modules. BioMove simulates a species' ability to occupy existing regions of climatic suitability realize newly available suitable climatic space as climate changes. As newly suitable area may be quite distant from existing distributions, BioMove represents the dynamic processes of demography, dispersal, disturbance, and competition for resources among plant functional types (PFTs) on the landscape

BioMove was initially tested for dynamic species modeling within California under a California Energy Commission project that concluded in 2008 (Hannah *et al.* 2008; CEC-500-2008-060). Four case studies of explored the dynamic distributions of subject species under projected 21 st century climate change. The case studies were designed to primarily capture the effects of probabilistic long-range dispersal as well as the interplay of the target species with representative plant functional types (PFTs) under climate change. The case studies made use of decadal climatic niche models at roughly 1km horizontal resolution.

Here we revisit three of those case studies (target species of *Pinus lambertiana, Yucca Brevifolia, and Quercus douglasii*) with updated species parameterization to reflect improvements in the demographic component and newly available finescale species niche models (90m - 800m horizontal resolution; see Chapter 3). Simulations are also designed more attention given to the effects of disturbance through refinements to the fire module that allows a more realistic

representation of the spatial distribution of fire probability as well as fine temporal scale variation in fire occurrences or intensity. In presenting the results of these simulations, we aim to demonstrate the evolved capabilities and potential applications of the model as well as to represent possible effects of climate change on prominent California plant species.

# 4.2 Revised BioMove Case Studies

# 4.2.1 Finescale Dynamic Model of *Pinus Lambertiana*, *Abies Concolor* and *Quercus Kelloggii* near LaTour Demonstration State Forest (90m resolution)

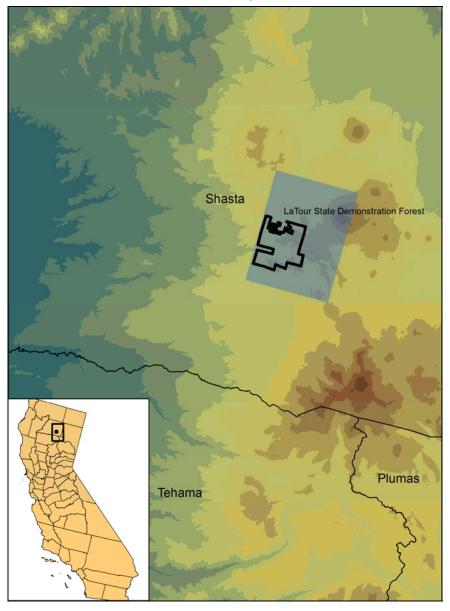
The three primary objectives of this simulation design were to 1) test the application of BioMove on recently completed species distribution models conducted at 90m horizontal resolution, 2) dynamical model the projected upslope migration of multiple species as climate envelopes along with shift with rising temperatures and 3) model the effects of fire in either facilitating or preventing species realization of climatic niche. The chosen study region was the mixed conifer forest surrounding LaTour Demonstration State Forest that bridges an elevation gradient from the northern Sacramento River valley to Lassen National Volcanic Range. Additionally, it is notable that all lands surrounding, LaTour, public or private, are managed for timber production. As a multi-use region that is positioned as a potential connectivity corridor within that is partially within state managed lands, the results of dynamic modeling have the potential to inform land use decisions and strategic conservation planning.

The dominant vegetation types found within the study area are mixed conifer and true fir. The mixed conifer type, which occurs at lower elevations and south-west facing slopes is characterized by white fir (*Abies concolor*) in association with sugar pine (*Pinus lambertiana*), ponderosa pine (*Pinus ponderosa*), and Douglas fir (*Pseudotsuga menzeii*). The true fir type, which occurs at upper elevations, is dominated by stands of white fir (*Abies concolor*) and red fir (*Abies magnifica*). Hardwoods that are also present in the system include Black oak (*Quercus kelloggii*) and big-leaf maple (*Acer macropylum*) (Beck and Rowe 2008).

As in the original case study appearing in the 2008 BioMove report, *Pinus lambertiana* (PILA) was chosen as the subject species because it represents the median of the elevational gradient and is present in both the mixed conifer type and the higher elevation true fir type. To represent the true fir type, occupying a climatic niche that overlaps with but is slightly above the target species, *Abies concolor* (ABCO) was parameterized as one PFT. *Quercus douglassii* (QUKE) was chosen as a second PFT to represent a sparsely occurring hardwood whose climatic niche is expected to expand upslope within the study region.

Figure 4.1: Location Map of LaTour Demonstration State Forest.

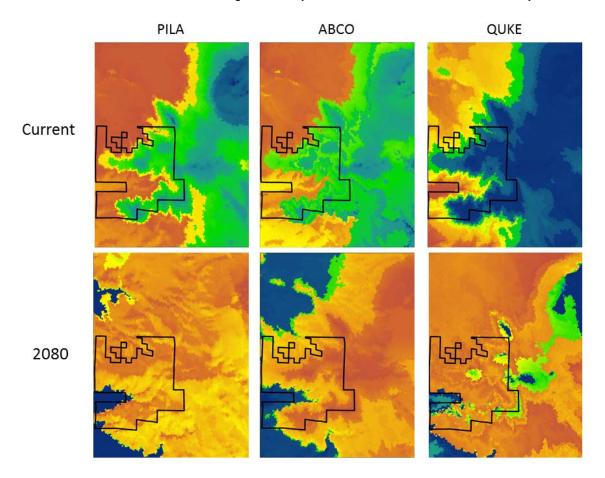
Rectangular Grid Used for BioMove Simulations is in Grey.



The modeled climatic niche surfaces that were used within the BioMove simulation for current, mid-century and end of century (GFDL; A2 emissions scenario) are depicted in Figure 4.2 where orange-red is high suitability and blue is low suitability. Decadal timesteps were used within the simulation, but three timesteps are shown here for clarity. It is evident that the climatic niche for all three species generally shifts from lower elevation (left) to higher elevations (right) with ABCO, PILA an QUKE occupying the highest, middle and lowest elevation zones respectively. With all three species gaining suitability in the center (middle elevations) of the study area by the end of the century, the simulation will examine how competition, demography, dispersal and disturbance will act in concert to dictate precisely how the procession may proceed.

Figure 4.2: Habitat Suitability Models for the Subject Species (PILA) and the 2 PFTS (ABCO and QUKE) for Current Climate and 2080 Climate GFDL Model A2 Emission Scenario.

Warm colors indicate high suitability whereas cool colors are low suitability.



#### 4.2.1.1 Parameterization

All three species represented in this simulation are long lived tree species with important differences regarding their susceptibility and resiliency to fire. The two PFTs (ABCO and QUKE) are distinguished in this simulation primarily by the strata of mature adults (ABCO = highest; QUKE = middle) and that QUKE has a greater capacity to survive and resprout after fire. ABCO has greater habitat suitability at higher elevations and is generally more prevalent in the initial conditions of the model. Both PFT species have an average age of 300 years and reach reproductive maturity after 20 years. Finally growth, recruitment, and mortality of both PFT species are constrained linearly by the habitat suitability model surfaces (Figure 4.2).

PILA, the subject species of the simulation, is an atypical subject species within the BioMove platform in that it co-occurs and occupies a similar functional type as one of the PFTs. However, PILA was retained as a subject species to allow it to respond differentially to varying intensities of fire as determined by the total PFT abundance on the landscape. In this simulation, PILA is able to germinate and juveniles can grow in low light conditions, but not in complete shade. Juveniles experience an annual mortality rate of 10 percent/year through 30

and adults are assigned an annual mortality rate of 2 percent year through an average reproductive age of 300 years (van Mantgem and Stephenson 2007). Mortality from fire at all age classes is limited for low intensity fires, but a majority of individuals are killed at higher intensity fires made possible by high combined abundance of PFTs. This reflects the observation that more recent stem densities have increased fire mortality among PILA as compared to historical conditions (Nesbin dissertation)

#### 4.2.1.2 Simulation

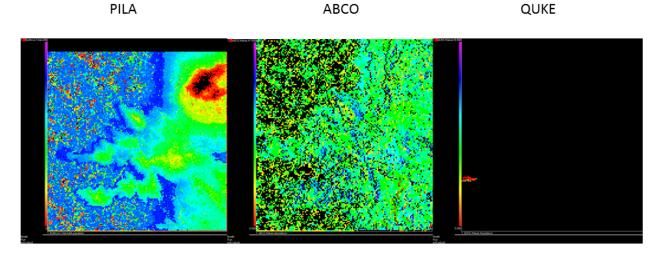
The target species and 2 PFTs were spun up in a blank landscape with modeled present climatic suitability surfaces controlling individual species demographics for 2200 years to achieve relative demographic stability and plausible spatial distribution of the three species (Figure 4.1). From there, the simulation was run for an additional 120 years with climatic suitability surfaces updated every ten years from 2000 - 2100. To investigate the role of disturbance in governing species range dynamics, the simulation was run both with and without fire.

#### 4.2.1.3 Results

As might be expected for long lived species that are prevalent on the landscape the shift in distribution over the 120 years of the simulation is subtle, but yet evident in the matrices of adult population at the conclusion of each run. Generally PILA is able to solidify lower elevation climate space due to the upslope displacement of ABCO as well as expanding into previously unrealized climate space at higher elevations. Although ABCO loses territory at lower elevations, the PFT is able to solidify mature abundance within existing true fir type areas at higher elevations. These general patterns hold from both with and without fire acting on the landscape.

Figure 4.3: Distribution of Mature Adults for All Three Species at the Conclusion of 2,200 Year Spin-Up Calibration.

Blues indicate high abundance where as red and black equate to low abundance and absence respectively.



Perhaps the most interesting player in this simulation is QUKE, whose initial distribution is limited to an isolated valley that is the lowest elevation within the study area. Without fire, QUKE is able to marginally expand its mature population range, but is still relegated to a small portion of the study area with much of its newly suitable climate space unrealized at the end of the simulation. However, when fire is allowed to act upon the landscape, QUKE is able to dramatically expand its range by virtue of its ability to colonize clearings created by fire that are now within the suitable climate space. The effect is more pronounced with either greater frequency or, enhanced severity/extent of fire. This notion of fire shepherding an oak into newly available climatic niche within dense conifer forest was also demonstrated in the 2008 report but reinforced here with the topographic and demographic realism afforded by habitat suitability models constructed with the 90m climate data.

Figure 4.4: Distribution of Mature Adults for All Three Species at the Conclusion of a 120 Simulation with Climate Change Shifting Modeled Habitat Suitability.

Blues indicate high abundance where as red and black equate to low abundance and absence respectively.

PILA

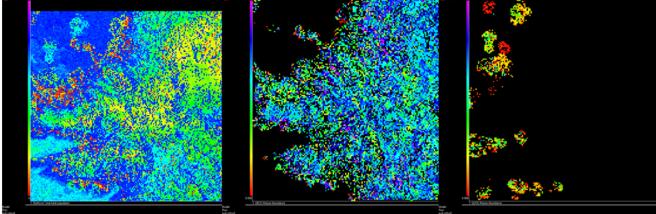
ABCO

QUKE

Figure 4.5: Distribution of Mature Adults for All Three Species at the Conclusion of a 120 Simulation with Climate Change and Fire Acting on the Landscape.

Blues indicate high abundance where as red and black equate to low abundance and absence respectively.

PILA ABCO QUKE



#### 4.2.1.4 Conclusions

This successful demonstration of a BioMove simulation with very fine scale climate data and a comparatively small spatial domain is an exciting and important refinement over earlier simulations. The successful colonization of newly available niche space of QUKE that is readily apparent at the conclusion of the 120 year simulation represents a migration on the scale of less than 10 km. Although this certainly represents a relevant change in a species range within a

managed area range dynamics at this scale may not be apparent in simulations conducted at coarser resolution over larger spatial domains. Continued development of potential case studies with fine scale climate data is a potentially valuable application of the BioMove platform to examine local scale species range dynamics.

# 4.2.2 Finescale Dynamic of *Yucca Brevifolia* in the Western Mojave Desert Ecoregion (270m Resolution)

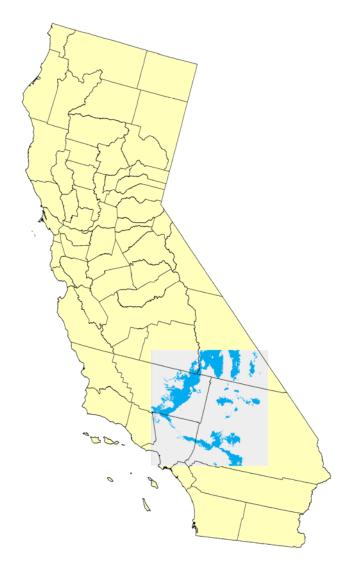
Yucca brevifolia (YUBR), or Joshua Tree, is perhaps the most recognizable and charismatic plant species of the Mojave desert ecosystem of California and Nevada. It is also widely identified as a species that is potentially vulnerable to climate change due to limited dispersal capacity and slow regeneration times. Several recent studies have identified existing populations of YUBR that are expected to be unsustainable as suitable climate space shifts both northward and upslope at a rate that outpaces maximum observed dispersal (Cole *et al* 2011; one more). Additionally, colonization of the Mojave ecoregion by invasive grass species (e.g. Bromus) may introduce heightened risk of fire which could suppress recruitment through increased juvenile and adult mortality. Indeed fire visitation when combined with drought has been observed cause 80 percent mortality among burned adult individuals (DeFalco *et al* 2010) illustrating the potentially profound impacts of climate change and fire on the long term viability of YUBR in the western Mojave desert.

The case study performed for the 2008 report also examined the effect of climate change on future YUBR distributions under differing scenarios of long-distance dispersal probability and fire visitation. Those simulations were conducted at 800m horizontal resolution and with decadal updates to habitat suitability surfaces under climate change. Refinements to that case study presented here include an updated demography, habitat suitability models constructed with 270m resolution climate data, increased fire mortality of mature adults per more recent observations, and realistic distribution of fire visitation based on a modeled fire probability surface. Use of the 270m resolution habitat suitability models, in particular, can help to address the question of whether climatic refugia that are capable of supporting persistent viable populations under climate change and increased risk of fire.

As available computing resources limit the effective scope of a simulation to 1,000 by 1,000 grid cells we were not able to dynamically model YUBR range dynamics at 270m resolution over the entire species range. The region of analysis selected for the simulation includes many of the core YUBR population within California with focus on the western Mojave desert (Figure 4.1). This region of analysis includes Joshua Tree National Park in the south as well as YUBR populations that are at potentially greater risk of invasion, fragmentation or fire due to proximity to populated areas.

Figure 4.6: Location Map of BioMove Simulation Area.

Square grid (1,000 x 1,000 cells) used for BioMove simulation shown below. Binary current distribution as modeled by Maxent at 270m resolution is shown in blue.



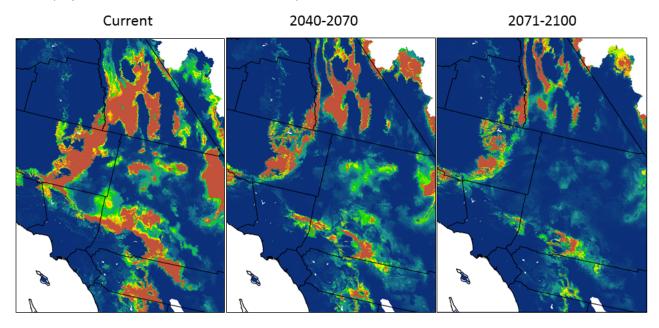
YUBR was parameterized according to values from published demographic and dispersal observations as well as recently contributed fire mortality statistics. Juveniles occupy the lowest strata and progress through 10 consecutive juvenile classes with 70 percent mortality at each step. This results in a juvenile pool that produces roughly 1 mature adult per 100 successful germinant – reflective of rare episodic recruitment events that are not well quantified (Esque *et al* 2010). Mature adults produce 150 viable seeds per year and are structured to live an average of 200 years with 2 percent annual mortality. Dispersal is given multiple experimental treatments described below, but is characterized by a mean dispersal distance of 100m. This is, in fact, a generous assumption as the maximum recorded dispersal of YUBR seed is 251 meters

(Lenz 2001). Long distance dispersal events are turned off to emphasize the limited dispersal capacity.

Updated habitat suitability surfaces due to climate change (GFDL; A2 emissions scenario) were imposed at decadal timesteps through 2100. The general northward shift of suitability and substantial decline of suitable climate space in the southern portion of the species range is evident in Figure 4.2. The simulation will aim to see the extent to which YUBR is able to persist within climatic refugia or colonize newly available climate space both with and without fire acting on the landscape.

Figure 4.7: Modeled Habitat Suitability (270m Resolution) for *Yucca Brevifolia* at Three Time Steps Where Red-Orange is High Suitability and Blues Are Low Suitability.

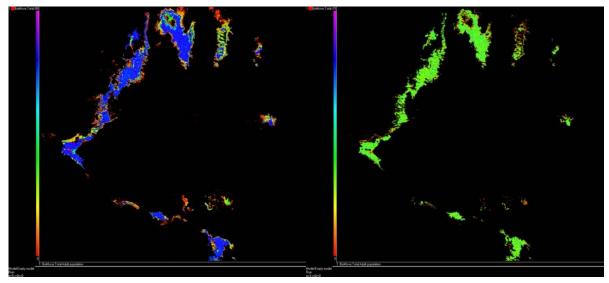




To calibrate the model, initial YUBR distribution within the study area was restricted to Maxent modeled current binary distribution. We then spun the model up for 1,000 years to attain a stable population with a mix of cohorts among seedlings, juveniles and reproducing adults. To focus modeling effort on YUBR distribution alone, we did not include any PFTs that would otherwise limit light resources or enable fire visitation. Instead, fire visitation was decoupled from landscape susceptibility and introduced via random initiation as well as a modeled fire probability surface. A fire visitation results in appreciable mortality for all age classes, killing 80 percent of adults and 95 percent of juveniles that are present. All treatments of fire and dispersal were all run for 120 years, representing the period 2000-2120.

Figure 4.8: Current BioMove Spin-Up (Left) and Future YUBR Adult Population after 120 Years (Right).

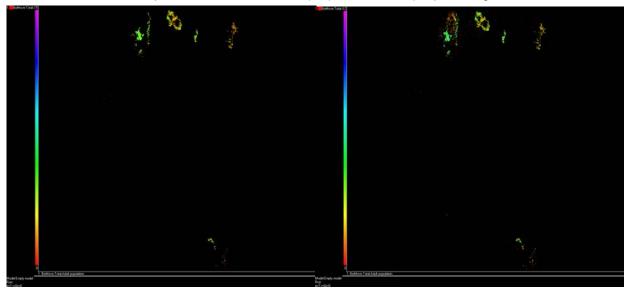
No climate change no fire. Purple and blue indicates high population density whereas red represents few individuals.



The initial simulation of YUBR on a blank landscape with no assumed climate change and no fire visitation shows that the species is demographically able to sustain populations in all current areas of climatic suitability, although there is an appreciable decline in the population density. Figure 4.3 shows the counts of reproducing mature adults per pixel both at the beginning of the simulation and at the end of 120 years of demographic processes alone. The decline in population density over 120 years is compatible with the narrative that YUBR distribution is not currently in equilibrium with suitable climate space and is already on a declining trajectory from its more expansive historical range (Cole et al 2011).

Figure 4.9: YUBR Adult Population after 120 Years under GFDL A2 Climate Change.

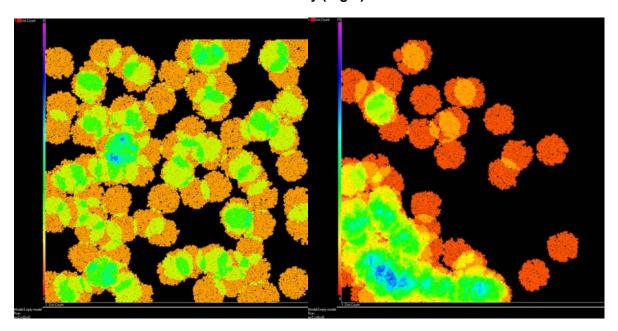
No disturbance. Mean dispersal distances of 100m (left) and 6,750m (25 pixels; right.



When projected 21st century climate change is imposed, remaining mature adults are relegated to the northern range of suitable climate space and restricted high elevation sites of the San Gabriel Mountains to the south. This redistribution pattern is consistent regardless of dispersal assumption. Although there are minor differences in the adult distribution maps between a realistic 100m dispersal assumption and an implausible 6,750m (equivalent to 25 pixels), it is clear that climate change and demographics are the primary driving forces in determining the ultimate distribution of YUBR this simulation.

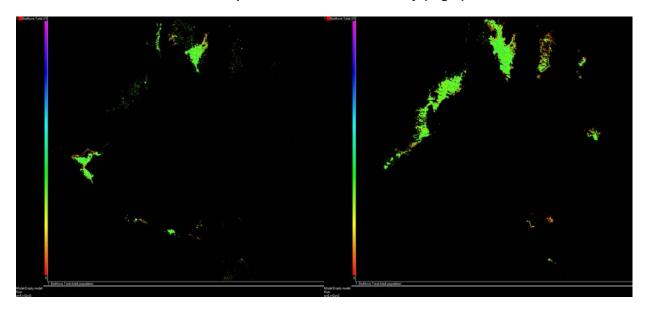
To examine how fire will interact with climate change in shaping YUBR range dynamics and to apply refinements of spatial realism to the fire module, we introduced fire to the landscape through two methods. First, fire initiation events at a constant rate of 1 imitation per year were allowed to occur randomly on the landscape. As there are no PFTs present on the landscape to control the rate of spread, fires were then extinguished after 1000 pixels burned - equivalent to roughly 73 km² or 18,000 acres. For the second method, fire initiation events were constrained by a class map modified from a modeled fire probability surface (Krawchuk and Moritz 2012). This serves to realistically concentrate the impacts of fire in regions that are known to have greater probability of fire visitation. Maps of the fire visit count for each fire treatment over the 120 year simulation are shown in Figure 4.5 with orange indicating few visits and blue indicating many visits. It is clearly evident that imposing the fire probability surface effectively constrains fire occurrences to the comparatively fire prone slopes of the central Transverse Ranges. This, in turn, will appropriately place greater risk of fire on the southern portion of YUBR distribution.

Figure 4.10: Count of Fire Visits under Random Distribution (Left) and Class Map of Modeled Fire Probability (Right).



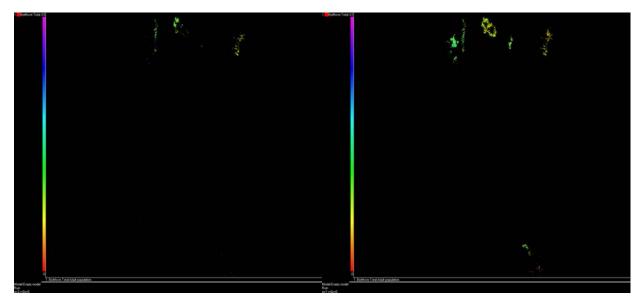
The two fire treatments offer contrasting outcomes on dynamic modeling of future YUBR distributions. Maps of reproducing adult distribution at the conclusion of each 120 year simulation without climate change show a greater decline of southern YUBR populations coupled with greater stability in northern populations in the simulation that included the fire probability surface (Figure 4.6). Conversely, random fire imitations leave some portions of southern range intact while impacting northern populations that are able to persist under probabilistic fire.

Figure 4.11: YUBR Adult Population after 120 Years under Random Fire Distribution (Left) and Class Map of Modeled Fire Probability (Right).



When decadal climate change is also imposed along with each of the fire treatments, the effects are more pronounced with only a small portion of the existing range retained through the end of the simulation (Figure 4.7). As before, when fire imitation is realistically constrained to southern portions of the study region, more reproducing adults are able to persist in regions of climatic suitability at the northern edge of the study area. The ultimate distribution of reproducing adults under probabilistic fire is similar to the climate change only simulation depicted in Figure 4.4, and is a more optimistic outcome for YUBR persistence under climate change. This result emphasized the importance and potential utility of incorporating such spatially explicit disturbance surfaces within the dynamic simulation platform the BioMove provides. This application will be further explored in the next case study: a distribution-wide simulation of Blue Oak (*Quercus douglasii*).

Figure 4.12: YUBR Adult Population after 120 Years under Random Fire Distribution (Left) and Class Map of Modeled Fire Probability (Right) – GFDL A2 Climate Change.



# 4.2.3 Statewide Dynamic Model of *Quercus Douglassii* with Spatially Explicit Probability Surface (800m Resolution)

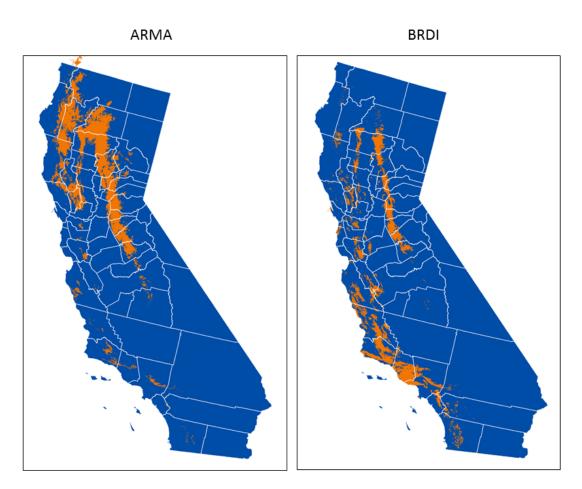
The final case study presented here is a distribution wide simulation of Blue Oak (*Quercus douglasii*) with attention given to the spatial distribution of fire on the landscape and its subsequent role in shaping Blue Oak distribution. The previous PIER funded BioMove also assessed Blue Oak, dividing the range into areas of expanding climatic suitability in the north and areas where suitability is projected to decline in the south. Those simulations revealed a general lack of success in terms of Blue Oak's ability to realize newly available niche space due to competition with conifer functional types. This simulation aims to explore the extent to which fire also impacts Blue Oak range dynamics under climate change.

As with the previous case study of Yucca brevifolia the effects of fire are tested with both a random distribution and a distribution tied to a statewide fire probability surface. A distinguishing feature of this case study is that propagation and intensity of fire is controlled by the presences of 3 PFTs on the landscape. This creates a landscape where even the random distribution fire treatment, fire severity (size and intensity) is governed by the distribution of the PFTs. PFTs include in the simulation to regulate fire in Blue Oak communities include two fire prone brush species, represented by *Artcostaphylus manzanita* (ARMA) and Artemesia californica (ARCA). ARMA is serotinous and therefore dependent upon repeated fire visits to germinate. ARCA is not fire dependent and is included to primarily add abundance and fire susceptibility the landscape where ARMA is not successfully established. Both species were initially confined to the modeled binary distribution of ARMA, which is coincident with much of the northern Blue Oak range. Dynamic processes in BioMove serve to then modify the distributions of each species as the model is spun up to achieve a stable system.

To provide fire prone vegetation and a source fire susceptibility to the southern portions of Blue oak range, a grass species represented by *Bromus diandrus* (BRDI) was included as the third PFT.

As with the shrub species, the BRDI PFT was initially constrained to the modeled binary distribution (Figure 4.13). The model was spun up for 1500 year with fire enabled to achieve stable populations of all three PFTs. The distribution of mature reproducing adult Blue oaks at the conclusion of this spin up is shown in Figure 4.15. Experimental simulations described below were then run for an additional 150 years representing the period 2000-2150.

Figure 4.13: Initial Binary Distribution (Orange = Present; Blue = Absent) for *Artcostaphylus Manzanita* and *Bromus Diandrus* 



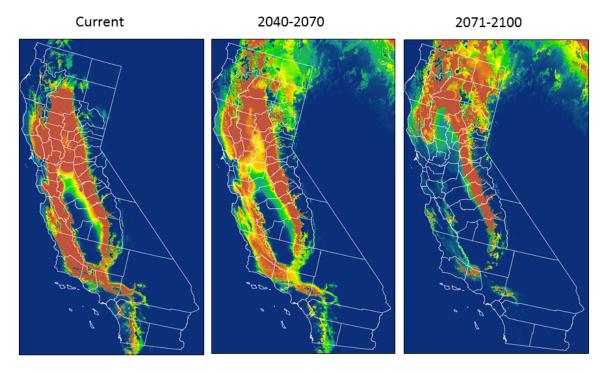
Habitat suitability models at 800m resolution (GFDL; A2 emissions) are imposed at decadal timesteps to reflect shifting climatic suitability under climate change. The suitability surfaces for current, midcentury (2040-2070), and end of century (2071-2100) time period are shown in figure 4.14 where red-orange is high suitability and blue is limited suitability. The rectangular image of each timestep also represents the extent of the grid used within the BioMove emulation. Under this climate scenario, there is an obvious and dramatic northward shift in climatic suitability for Blue Oak. By the end of the century, much of the existing range in the foothills surrounding the southern central valley is lost, particularly the western flank of suitability in the southern Coast and Temblor ranges. This rapid redistribution of suitable

climate, coupled with infrequent, episodic recruitment events render Blue Oak a potentially vulnerable species under climate change.

Blue Oak is parameterized to reach reproductive maturity after 30 years with germination and juvenile mortality rates explicitly tied to habitat suitability. Juveniles experience a significant mortality rate, even in most favorable habitats of 50 percent per year. Mature adults are less affected by climate envelope, but the least suitable habitats (blue and green in Figure 4.14) do impose additional mortality. In the best habitats, mortality among adult individuals is approximately 0.5 percent per year whereas poor habitats increase adult mortality to 4-5 percent per year. This mortality range is in line with published estimates of Blue Oak mortality by all causes of 2-3 percent per year (Tyler *et al.* 2006). Dispersal is assumed to be a mean of 30m per year (Johnson et al 2009), with 1 percent of seeds reserved for long distance dispersal (maximum throw of 2.4km or 3 pixels). All age groups are impacted by fire, with adults experiencing reduced mortality in low intensity fires and the ability to resprout as a sub-adult in all but the most intense fires. Again, fire intensity is controlled by the combined susceptibility and abundance of PFTs on the landscape – and is independent of Blue Oak abundance.

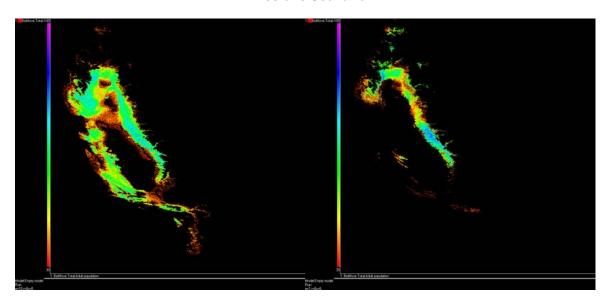
Figure 4.14: Modeled Habitat Suitability (800m Resolution) for *Quercus Douglasii* at Three Time Steps Where Red-Orange Is High Suitability and Blues Are Low Suitability.

Future projections are based on GFDL GCM output under the A2 emissions scenario.



The results of the 150 year simulation under climate change are depicted in 4.15. The effect of the climate envelope on recruitment and mature adult mortality is sufficient in this simulation to extirpate Blue Oak from the southern and western portions of its modeled range. Due to infrequent long distance dispersal events and the presence of highly suitable habitat at the conclusion the simulation, Blue oak is successfully able to colonize or solidify adult populations in patches that are currently to the north and east of the modeled distribution. As this simulation does not include a conifer PFT, Blue Oak is not competing for light resources in these areas, and thus has a very favorable path to establishment that may be an over-optimistic representation of reality.

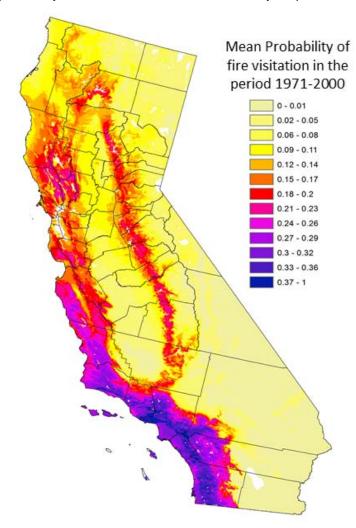
Figure 4.15: Final Distribution of Mature *Quercus Douglasii* after 150 Years of No Climate Change (Left) and Decadal Updates of Habitat Suitability Based on GFDL GCM Output under the A2 Emissions Scenario.



The fire probability surface that is used to spatially constrain initiations is modified for BioMove from data produced and presented in the PIER funded report (Krawchuk and Moritz 2012). The modeled mean probability of one fire occurrence over the 30 year period 1971-2000 is shown in Figure 4.16 where purple is greater likelihood of occurrence and yellow is low fire probability. To incorporate this information into the BioMove fire module, it must be converted to a class map that divides the model domain into regions that contribute varying percentages to the total number of fire initiations. We created this class map by creating 5 equally spaced bins of probability values and assigning increasingly greater percent contribution so that the lowest probability areas (light yellow in Figure 4.16) account for 1 percent of all ignitions and the areas of highest probability (purple in Figure 4.16) contribute 30 percent of all ignitions. The choice of class breaks and percent contribution was provisional and meant to capture the general distribution of fire prone regions in California. Subsequent refinements to the values given to each class could provide for a more highly resolved representation of fire probability.

Figure 4.16: Fire Probability Surface Used to Control Fire Initiations (Data from Krawchuk and Moritz 2012).

Data shows the mean probability of one fire occurrence over the 30 year period 1971-2000



To test the impact of including spatially explicit information regarding fire occurrences, we performed the identical 150 year simulation with three distinct fire treatments under climate change. First, fire ignitions were allowed to occur randomly on the landscape with an independent probability of propagation set to 32 percent. Alternatively, fire initiations were constrained to the class map described above and propagation was again controlled by the PFTs. Maps of the final mature Blue Oak populations and fire visit counts for each treatment are presented in Figures 4.17 and 4.18. Areas where major fire occurrences have appreciably altered the final distribution of adult Blue Oaks as compared to the climate change only simulation (Figure 4.15; right panel) are highlighted by white circles.

Figure 4.17: Final Distribution of Mature *Quercus Douglasii* and Visitation Assuming Random Fire Initiation Locations.

Areas of fire impact are highlighted by white circles.

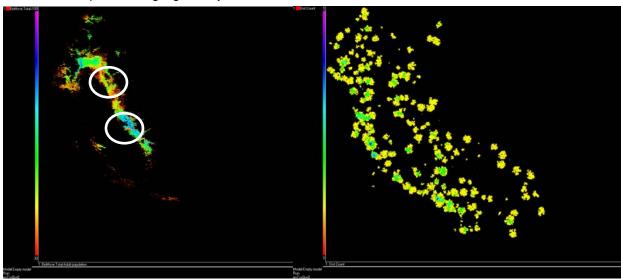
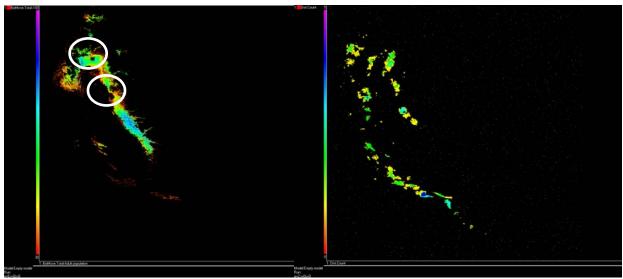


Figure 4.18: Final Distribution of Mature *Quercus Douglasii* with Fire Visitation Controlled by Spatially Explicit Probability Surface.

Areas of fire impact are highlighted by white circles.



In both cases, it is clear that in this simulation, the climate envelope is the driving force in determining the final distribution of mature adults (left panels in Figures 4.17 and 4.18). Additionally, in both treatments, fire visits do create gaps in the Blue Oak distribution within fire prone regions of the Sierra foothills. However, the map of fire visits where ignitions are controlled by the fire probability surface (right panel; Figure 4.18) demonstrates a greater conformity to known fire prone regions of California and greater coincidence with existing Blue Oak distribution. Unlike the YUBR case study described above, incorporation of the fire probability surface does not have a profound effect on the final distribution of Blue Oaks in this

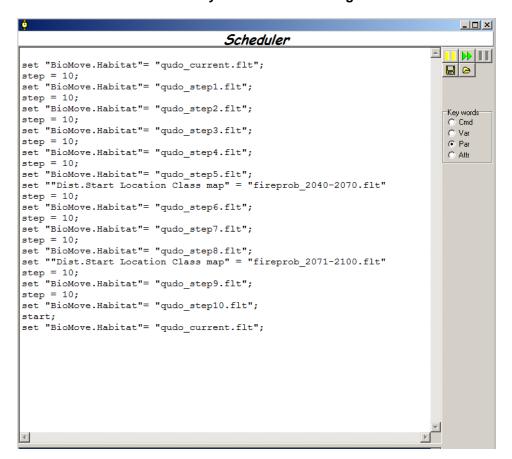
simulation. Yet, the benefits of adding plausibility and realism to fire visitations in modeling fire prone species over large spatial domains are clearly illustrated and represent an important development in the application of BioMove within California

#### 4.3 Refinements to Fire Disturbance Module

## 4.3.1 Inclusion of Modeled Projections of Fire Probability under Climate Change

The inclusion of the modeled fire probability surface produced and presented in the PIER funded study Krawchuk and Moritz 2012 provides valuable realism to the spatial distribution of fires in BioMove simulations. The probability surface included in the two simulations presented above represents fire probability for the thirty year period 1971 – 2000. To further refine the representation of fire on the landscape under climate change and to account for potential climate change impacts on fire probability, it is possible to include modeled future fire probability surfaces using the scheduler function. An example script that demonstrates one possible method of updating fire probability as well as climate change is show in Figure 4.19.

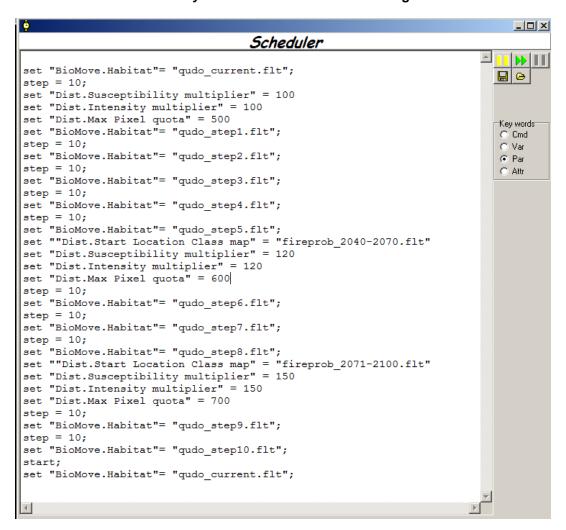
Figure 4.19: Example Script in the BioMove Scheduler Window to Update Class Maps of Fire Probability under Climate Change.



Probability surfaces were produced statewide at 1080m horizontal resolution for two GCMs, two emissions scenarios and multiple scenarios of urban expansion. Incorporation of these various scenarios of fire distribution will be valuable in capturing a full range of possible outcomes for species on a fire prone landscape and is an important opportunity for future

research and application of BioMove. It is also important to note that the fire probability surfaces serve only to control the locations of fire initiation. Additional modifications that will either increase or decrease the severity of fire (in addition to dynamic interactions of PFTs on the landscape) can also be imposed with the scheduler scripting window. An example of how create more intense and larger fires under climate change is shown below in Figure 4.20.

Figure 4.20: Example Script in the BioMove Scheduler Window to Increase Fire Susceptibility, Intensity and Extent under Climate Change.



# 4.3.2 Methods to Account for Sub-Annual Variation in Fire Probability

The BioMove platform is designed to interpret model steps as yearly intervals. All of the case studies presented above rely on this yearly timestep assumption in the values used for parameterizing the demographic module, PFT life history traits, and decadal updates of the habitat suitability surfaces used in climate change scenarios. However, representation of dynamic landscape processes may be improved by incorporating finer temporal scale variation in both climatic suitability and the disturbance modules. Annual or sub-annual variability of climatic suitability according to simple random variation about the mean or longer term cycles is a direction of future research. Additionally, similar fine temporal scale variation in the

initiation and propagation of fire has the potential to better resolve the role of fire in species range dynamics. Here we present methods to account for sub-annual (seasonal) variation in fire occurrences. The fine scale Pinus lambertiana case study in LaTour Demonstration State Forest will serve as an illustration of the implementation of such refinements to the fire module.

Fire occurrences within California progress through a natural cycle of high fire activity in the summer months and low activity in the cooler, wetter winter months. To represent this annual cycle, we will modify the LaTour simulation so that each year is split into six time steps. Fire activity will then follow an initiation function that reflects the annual variability of fire. The first and essential step to modify a simulation to account for seasonal cycles in fire probability is to modify the demographic module for the subject species as well as the life history tab for each of the PFTs. For the life history tab, this is simply multiplying the annual parameters by the new number of sub annual timesteps (e.g. a species that lives 300 years and matures after 20 years will be modified to 1800 timesteps and 120 timesteps respectively). Modifying the demographic parameters requires that the compounding mortality rate be converted to a fractional rate so that when the new rate is raised to the power of the number of sub-annual timesteps it equals the original annual mortality rate or  $[(1-R_1) = (1-R_2)^n]$ . As an example, modifying a 10 percent annual mortality rate to six sub-annual timestep (n=6) equivalent of 1.74 percent can be accomplished through the following steps:

```
(1-R_1) = (1-R_2)^6

ln(0.9) = 6 * ln(1-R_2)

-0.01756 = ln(1-R_2)

e^{-0.01756} = 1-R_2

0.9826 = 1-R_2

R_2 = 0.0174
```

Once the demographic parameters have been modified, the next step is to impose a periodic frequency function on fire initiation to reflect seasonal variability. This is easily accomplished in the disturbance initiation tab where one is able to set the period and range of a variability cycle. For this example, we will set the period to six sub-annual timesteps and the range to two so that six disturbances per year will be initiated (Figure 4.21).

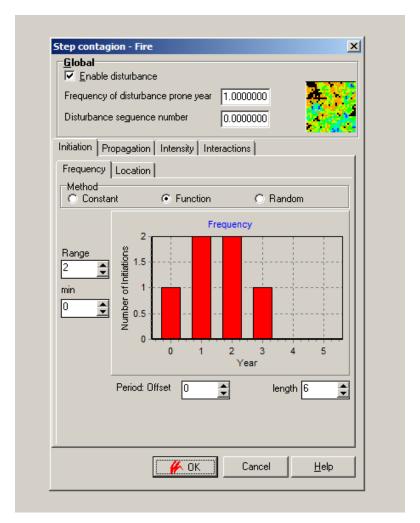
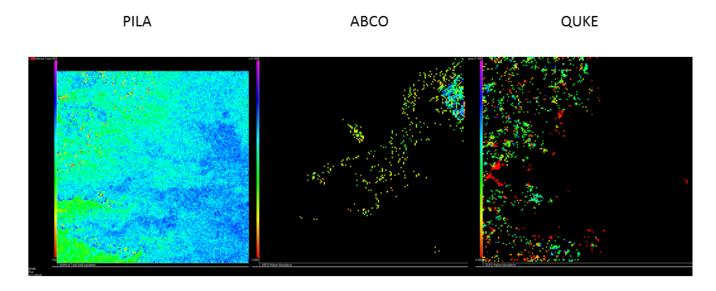


Figure 4.21: Example BioMove Dialogue Window to Control Periodicity of Fire Initiations.

The result of applying this sub-annual variation in fire frequency within the Pinus lambert Ian simulation in LaTour is significant and somewhat surprising. As Figure 4.22 illustrates, the prevalence of both PILA and QUKE at the conclusion of the simulation is enhanced by the inclusion of sub-annual variation (compare to Figure 4.5). Conversely, final ABCO distribution is greatly reduced, with mature individuals to the highest elevations in the study area. It is evident that the fire free periods representing the winter months allow PILA a greater opportunity to establish in all areas of high habitat suitability. Likewise, the pulses of high fire activity in the summer months provide enough openings in the ABCO for QUKE to germinate and realize large new portions of modeled niche space.

Figure 4.22: Final Distributions of Mature Adults for Each Species for 720 Time Step (120 Years) Including Sub-Annual Variability of Fire Visitation.



It is clear that the incorporation of sub-annual fire variability has the potential to appreciably alter the outcomes of a given simulation. An interesting next step and topic for future research would be to also incorporate fine temporal scale updates to habitat suitability surfaces. Imposing variability functions on habitat suitability surfaces could afford the potential to test the effects of multi-year phenomena such as El Nino or Pacific Decadal Oscillation as well as seasonal variations in conditions in temperature and precipitation. Dynamic modeling of such sub-annual variation may provide insight as to the conditions that create episodic windows of recruitment for long-lived species and how those conditions may be affected by climate change or heightened disturbance.

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# APPENDIX A: Documentation of CPNF R Package (Version 06.16)

R Documentation:

Conservation Prioritization using Network Flow (cpnf)

Author(s)

Oliver Soong

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## Description

Implements a conservation prioritization algorithm based on network flow. There is a function to export the problem in CPLEX LP format for use with external linear programming software packages. There are additional functions for integration with Gurobi.

**Details** 

Package: cpnf

Type: Package

Version: 0.6-16

Date: 2012-06-07

Species conservation efforts must balance multiple priorities with limited resources. Climate change is expected to introduce range shifts, rendering existing optimization approaches insufficient. One way to handle the more complex optimization under climate change is the network flow approach (Phillips et al. 2008). A general introduction to network flow and linear programming is beyond the scope of this overview, although there are many books available on the subject (e.g., Bazaraa et al. 2009).

At its core, this approach takes as input maps of suitable habitat and conservation cost and selects candidate areas for protection. These candidate areas are selected such that species are able to disperse from suitable habitat at one point in time to suitable habitat at a future point in time. Broadly, most typical conservation prioritization problems can be simplified into two

roughly symmetric problems, namely minimizing cost for a fixed benefit and maximizing benefit for a fixed cost.

What is meant by conservation cost and benefit? Conservation cost is usually the cost of land acquisition, although this approach can sensibly deal with other measures of cost. Whereas conservation benefit has traditionally been measured as some function of area and species richness, the functions provided in this package measure conservation benefit as the total area of protected "chains", defined below. This is a limitation of the current version of this package that is not inherent to the approach in general.

It is perhaps easiest to explain a "chain", by example. Consider *Monardella sheltonii* and modeled suitable habitat in 2000, 2010, and 2020. We begin with a 1 square kilometer patch of suitable habitat in 2000. A 1 square kilometer link in the chain comprises this 1 square kilometer in 2000 and another 1 square kilometer of modeled suitable habitat in 2010 that is close enough that propagules of *Monardella sheltonii* can disperse from one patch to the other in the duration between 2000 and 2010. Naturally, a 1 square kilometer chain from 2000 to 2020 comprises a link from 2000 to 2010 and another link from 2010 to 2020. These chains are of conservation interest only if the suitable habitat is protected. It is worth noting that the patches in the chain may comprise the same spatial location, such as when modeled distributions for a species do not change much. It is also worth noting that overlapping chains, which share a patch of suitable habitat in some year, are of less conservation value than similar non-overlapping chains.

There are a number of practical considerations to be aware of when conducting a network flow analysis. In the case of the minimization problem, the goal is to minimize the cost of achieving some pre-defined conservation benefit. The pre-defined benefit is usually simple (e.g., all species must have 100 square kilometers of protected chains). Defining this fixed conservation benefit is complicated by the fact that some species may not be capable achieving the pre-defined benefit, no matter how much land is conserved. In such a case, the linear programming/network flow problem has no feasible solution. It is possible, however, to determine the maximum number of chains a species can achieve by solving the maximum benefit problem for that species alone, using an infinite cost limit (i.e., larger than the total cost of protecting all pixels).

When dealing with many species, it is useful to reduce the complexity of the problem. In some cases, species can be protected using existing protection alone, such that it is unnecessary to acquire additional conservation lands for the sole purpose of protecting these species. In other words, some species are able to form enough chains to achieve any conservation targets using existing protected areas alone. It is possible to identify these species by solving the maximum benefit problem for each species individually, using a 0 cost limit.

This package provides exportLP, which writes the conservation prioritization problem as a CPLEX LP formatted file (possibly compressed). The generated file may be read and solved using any of the many linear programming solvers available. This package, however, has convenience functions dolp, which invokes the Gurobi optimizer, and readSol, which imports the solution into R. To assist with visualization of this solution, the functions makeChains and makeRaster generate GIS outputs of the dispersal linkages and areas selected for protection.

Gurobi must be installed separately, but it is not required to use exportLP or solve the problems it outputs. Although R can handle gzip and bzip2 files natively, Gurobi needs the corresponding program to be installed and accessible via the system path. This package has only been tested with Gurobi 5.0.0, although other versions may work as well.

Run Exported Problems using Gurobi

doLP {cpnf}

# Description

Use Gurobi's command-line interface to solve exported cpnf problems.

## Usage

# Arguments

A cpnf object, containing a description of the exported cpnf problem. This

is usually obtained from exportLP.

gurobi character, the location of gurobi\_cl.exe. By default, this function searches

in the path defined by the environment variable GUROBI\_HOME.

gurobi.parameters named list, parameters to be passed to Gurobi. Parameters should be name-

value pairs, along the lines of list(GurobiParameter1 = "Text

Value", GurobiParameter2 = Number).

compress character, one of "none", "gzip", "bzip2", or "same", describing the

compression Gurobi should apply to the solution output. See Details

regarding "same".

outdir character, output directory for solution files. By default, uses the same

directory as the exported cpnf file. Gurobi must be able to write files to this

directory.

# **Details**

This function instructs Gurobi to write its output to the directory specified by outdir. It is possible to tell Gurobi to write the log and solution files to different locations using qurobi.parameters.

Setting compress to "same" means to use the same compression that the 1p was exported with.

Gurobi must be installed for this function to work. For larger problems, it can be helpful to use compressed files, but to do this, Gurobi requires the appropriate compression tool be installed and accessible via the system path.

#### Value

Invisibly returns a modified copy of the 1p parameter, with additional components:

```
gurobi.compress a copy of the compress parameter used for the solution output gurobi.parameters a copy of the gurobi.parameters passed to Gurobi
```

See Also

http://www.gurobi.com, http://www.gurobi.com/doc/40/refman/node572.html for parameter help

### Examples

```
data(cpnf example)
costs <- 0:1
fixed.constraint <- c(Allium bolanderi bolanderi = 9.1, Monardella sheltonii
dispersal.range <- c(Allium_bolanderi_bolanderi = 0.15, Monardella_sheltonii
layer.names <- layerNames(speciesMaps)</pre>
mapInfo <- data.frame(matrix(unlist(strsplit(layer.names, "\\.")), ncol = 2,</pre>
byrow = TRUE))
names(mapInfo) <- c("species", "time")</pre>
mapInfo$time <- as.numeric(levels(mapInfo$time))[mapInfo$time]</pre>
mapInfo$index <- 1:nlayers(speciesMaps)</pre>
lp <- exportLP(direction = "minimize", speciesMaps = speciesMaps, mapInfo =</pre>
mapInfo, costs = costs, costStack = costStack, fixed.constraint =
fixed.constraint, dispersal.range = dispersal.range, name = "cpnf example")
## Not run:
lp.run <- doLP(lp)</pre>
## End(Not run)
```

Core Export Function

exportLP {cpnf}

Description

Write a conservation prioritization problem using the network flow approach as a linear programming problem in a (possibly compressed) CPLEX LP formatted file. The exported CPLEX LP file can be read using most standard linear programming solvers, although this package is designed to work with the Gurobi optimizer.

## Usage

```
exportLP(
          direction = c("minimize", "maximize"),
          speciesMaps,
          mapInfo,
          costs,
          costStack,
          fixed.constraint,
          dispersal.range,
          binary,
          name,
          compress = c("none", "gzip", "bzip2"),
          overwrite = TRUE,
          outdir = "."
)
```

### Arguments

direction

character, one of "minimize" or "maximize", indicating whether to minimize cost given a fixed benefit or to maximize benefit for a fixed cost

speciesMaps

object coercible to RasterStack, containing suitable habitat maps indicating the proportion of a given pixel that is suitable habitat for a given species.

Typically, this is a character vector of filenames. See Details.

mapInfo

data.frame describing the maps, containing at least three columns:

character or factor, distinguishing a unique species (including species true species, subspecies/varieties, or species-scenario combinations)

time numeric, modeled time of the map

numeric or integer, which layer of speciesMaps corresponds to index this species and time. NA values indicate the row should be ignored.

costs

numeric of length equal to the number of layers in costStack, containing the cost of acquiring the areas indicated in the corresponding layer of costStack.

costStack

object coercible to RasterStack, containing maps of the proportion of each pixel that can be acquired for the costs given in costs. Typically, this is a character vector filenames of the maps. See Details.

fixed.constraint When minimizing cost, this is a numeric vector of fixed benefits, which are the desired numbers of chains for each species. Names should correspond to

mapInfo\$species. When maximizing benefit, this is a single numeric, the

fixed cost (cost limit, really), in the same units as the cost map.

dispersal.range named numeric, containing the dispersal range (in pixels per unit of

mapInfo\$time) of each species, with names corresponding to

mapInfo\$species.

binary logical/boolean, define the binary problem, in which pixels are either

entirely protected or not.

name character, problem name and also output file name. This function will tidy

the file name for the computer to understand.

compress character, one of "none", "gzip", or "bzip2", describing the compression to

use when writing the exported problem. See Details.

overwrite logical/boolean, overwrite output file if it already exists.

outdir character, output directory, which will be created if necessary and must be

writable.

#### **Details**

The relationship between speciesMaps and mapInfo can be confusing. mapInfo tells this function which layers of speciesMaps to use and what species and year those layers represent. In a simple case, speciesMaps is a vector of filenames, mapInfo is a data.frame with one row for each file in speciesMaps, and mapInfo\$index is the trivial sequence 1:nrow(mapInfo). More complex arrangements are possible. For some users, it might be easier to create mapInfo in an external program and read this into a data.frame in R.

Suitable habitat, in this context, indicates areas that, if acquired for protection, would provide habitat benefit for that species. Fractional values allow for situations in which only a portion of a pixel comprises suitable habitat (e.g., a pixel is half suitable habitat and half developed). In other words, a pixel value of 0.3 in a particular layer of speciesMaps means that 30 percent of that pixel is suitable habitat for the species and time represented by that layer.

It is worth pointing out that species distribution models usually only indicate bioclimatic suitability, but areas that are bioclimatically suitable may not actually be suitable habitat for many reasons, such as land conversion and development. It is generally necessary to decrease the area of suitable habitat determined by bioclimatic distribution models before use in this function.

At present, the algorithm assumes that within-pixel suitable habitat is nested. In other words, it is currently assumed that areas acquired for protection within a pixel will be suitable for all species that have any suitable habitat within that pixel (limited, of course, by the total amount of suitable habitat of that species within that pixel). In other words, if 50 percent of a pixel is suitable for species A and 70 percent is suitable for species B, and if 60 percent of that pixel were acquired for protection, then 50 percent of the pixel is assumed to be protected suitable habitat for species A and 60 percent of the pixel is assumed to be protected suitable habitat for species B. At present, if this assumption is problematic, the only solution is to conduct a finer-scale analysis.

Similar to fractional suitable habitat, multiple layers of pixel costs allow for some areas within a single pixel to have different acquisition costs from other areas within the same pixel (e.g., half of the pixel is unprotected suitable habitat and half is already protected/free to acquire). In other words, a pixel value of 0.2 in a particular layer of costStack indicates that 20 percent of the pixel can be acquired for the cost given by the corresponding entry of costs.

Maps and datasets of land costs may not include information on potentially substantial existing protection in the form of parks, preserves, and conservation easements. These can generally be represented as having zero cost, but such adjustments must be made to the cost map before input to this function.

speciesMaps, mapInfo, fixed.constraint, and dispersal.range may contain more entries than are necessary for the problem. Extraneous entries will be ignored.

This function can write a compressed file by setting the compress parameter, which can be useful for larger problems. However, for Gurobi to read the compressed file, the appropriate decompression tool must be installed and accessible via the system path.

#### Value

Invisibly returns a list describing the exported problem, with named components:

name	a copy of the original name parameter
tidyName	the output directory and a tidied copy of the original name parameter
compress	a tidied copy of the original compress parameter
lpFile	the tidied output file name
species	the names of the species in $mapInfo$species$ in order of the underlying species index$
costs	a copy of the original costs parameter
times	the sorted unique times in mapInfo\$time in order of the underlying time index
spatialIndex	a RasterLayer describing the spatial domain of the analysis but lacking values

# Examples

```
data(cpnf_example)
costs <- 0:1
min.fixed.constraint <- c(Allium_bolanderi_bolanderi = 9.1,
Monardella_sheltonii = 5.4)
max.fixed.constraint <- 25
dispersal.range <- c(Allium_bolanderi_bolanderi = 0.15, Monardella_sheltonii = 0.2)
# construct mapInfo</pre>
```

```
layer.names <- layerNames(speciesMaps)</pre>
mapInfo <- data.frame(matrix(unlist(strsplit(layer.names, "\\.")), ncol = 2,</pre>
byrow = TRUE))
names(mapInfo) <- c("species", "time")</pre>
mapInfo$time <- as.numeric(levels(mapInfo$time))[mapInfo$time]</pre>
mapInfo$index <- 1:nlayers(speciesMaps)</pre>
# minimization example
lp.min <- exportLP(direction = "minimize", speciesMaps = speciesMaps, mapInfo</pre>
= mapInfo, costs = costs, costStack = costStack, fixed.constraint =
min.fixed.constraint, dispersal.range = dispersal.range, name = "cpnf min
example")
# maximization example
lp.max <- exportLP(direction = "maximize", speciesMaps = speciesMaps, mapInfo</pre>
= mapInfo, costs = costs, costStack = costStack, fixed.constraint =
max.fixed.constraint, dispersal.range = dispersal.range, name = "cpnf max
example")
# subset example
lp.sub <- exportLP(direction = "min", speciesMaps = speciesMaps, mapInfo =</pre>
subset(mapInfo, species == "Monardella_sheltonii"), costs = costs, costStack
= costStack, fixed.constraint = min.fixed.constraint, dispersal.range =
dispersal.range, name = "cpnf Monardella_sheltonii min example")
```

Import Gurobi Solutions into R

readSol {cpnf}

## Description

Import solutions calculated by Gurobi into R for further analysis.

#### Usage

### Arguments

A cpnf object, containing a description of the solved cpnf problem. This is usually obtained from dolp or sometimes exportlp.

character, the location of the solution file to be read. By default, this function will examine 1p for the location of the solution.

compress character, one of "none", "gzip", or "bzip2", indicating the compression used on the output solution. By default, this function will examine 1p for the compression applied

to the solution file. It is only necessary to specify this parameter if solfile is provided.

#### **Details**

Typical usage is to provide the output of dolp, in which case the default behavior will determine the solution file and compression automatically. It is possible to specify the solution file and compression, which is useful when Gurobi was invoked without using dolp (in which case lp can be the output of exportlp) or when the solution file has been moved or renamed from when dolp was invoked.

#### Value

Invisibly returns a modified copy of the 1p parameter, with additional components:

gurobi.solution the location of the solution file that was read

objective	value of objective function, which is either the minimized cost or the maximized benefit, depending on the problem
pixels	data.frame, indicating the proportion of the pixel at each cost level that is selected for conservation
links	data.frame, indicating the flow along utilized chain links
costLinks	data.frame, indicating for each time and species the proportion of utilized pixels at each cost level that is used for flow

#### See Also

http://www.gurobi.com, http://www.gurobi.com/doc/40/refman/node572.html for parameter help

#### Examples

```
data(cpnf_example)
costs <- 0:1
fixed.constraint <- c(Allium bolanderi bolanderi = 9.1, Monardella sheltonii
dispersal.range <- c(Allium_bolanderi_bolanderi = 0.15, Monardella_sheltonii
= 0.2)
layer.names <- layerNames(speciesMaps)</pre>
mapInfo <- data.frame(matrix(unlist(strsplit(layer.names, "\\.")), ncol = 2,</pre>
byrow = TRUE))
names(mapInfo) <- c("species", "time")</pre>
mapInfo$time <- as.numeric(levels(mapInfo$time))[mapInfo$time]</pre>
mapInfo$index <- 1:nlayers(speciesMaps)</pre>
lp <- exportLP(direction = "minimize", speciesMaps = speciesMaps, mapInfo =</pre>
mapInfo, costs = costs, costStack = costStack, fixed.constraint =
fixed.constraint, dispersal.range = dispersal.range, name = "cpnf example")
## Not run:
lp.run <- doLP(lp)</pre>
```

```
lp.sol <- readSol(lp.run)
## End(Not run)</pre>
```

# Functions to Generate Solution Outputs

# Description

makeChains generates a SpatialLinesDataFrame with the individual links in the chains found in the solution.

makeRaster generates a RasterLayer showing the input data and the pixels selected for protection.

#### Usage

```
makeChains(lp)
makeRaster(lp)
```

Arguments

<sup>1p</sup> a solution obtained from the readSol function.

#### **Details**

Objects returned from these functions exist only in the R workspace. They can be exported to standard GIS file formats using the standard export functions (e.g., writeRaster or writeOGR).

#### Value

makeChains returns a SpatialLinesDataFrame containing the individual chain links with an attributes table:

```
species name of the species

startTime time at the start of the chain link

startX X coordinate of the start of the chain link

startY Y coordinate of the start of the chain link

endTime time at the end of the chain link

endX X coordinate of the end of the chain link

endY Y coordinate of the end of the chain link

flow flow along the chain link
```

makeRaster returns a RasterLayer containing the proportion of a given pixel that was selected for protection.

## Examples

```
data(cpnf_example)
costs <- 0:1
fixed.constraint <- c(Allium_bolanderi_bolanderi = 9.1, Monardella_sheltonii
dispersal.range <- c(Allium_bolanderi_bolanderi = 0.15, Monardella_sheltonii
= 0.2)
layer.names <- layerNames(speciesMaps)</pre>
mapInfo <- data.frame(matrix(unlist(strsplit(layer.names, "\\.")), ncol = 2,</pre>
byrow = TRUE))
names(mapInfo) <- c("species", "time")</pre>
mapInfo$time <- as.numeric(levels(mapInfo$time))[mapInfo$time]</pre>
mapInfo$index <- 1:nlayers(speciesMaps)</pre>
lp <- exportLP(direction = "minimize", speciesMaps = speciesMaps, mapInfo =</pre>
mapInfo, costs = costs, costStack = costStack, fixed.constraint =
fixed.constraint, dispersal.range = dispersal.range, name = "cpnf example")
## Not run:
lp.run <- doLP(lp)</pre>
lp.sol <- readSol(lp.run)</pre>
## End(Not run)
chains <- makeChains(lp.sol)</pre>
protection <- makeRaster(lp.sol)</pre>
if(require(rgdal)) {
  writeOGR(chains, ".", "cpnfExChains", "ESRI Shapefile", overwrite_layer =
TRUE)
  writeRaster(protection, "cpnfExProt.tif", format = "GTiff", datatype =
"FLT4S", overwrite = TRUE, options = "COMPRESS=LZW")
}
breaks \leftarrow seq(0, 1, length.out = 257)
image(protection, col = grey(255:0/255), breaks = breaks)
plot(chains, add = TRUE, col = rgb(1, 255:0/255, 255:0/255)[cut(chains$flow,
breaks)], lwd = 3)
box()
```